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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

March 30, 2005, 17:12:40 ; Search time 183 Seconds (without alignments) 170.693 Million cell updates/sec Run on:

US-10-719-623A-16 306 1 MFTLKKSLLLLFFLGTINLS......EVEKRFFPVIGRILNGILGK 61 Title: Perfect score: Sequence:

1612378 segs, 512079187 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	tempor	tempor	tempor	catesb	escule	rugosa	pipien	schmac	rugosa	pipien	pipien	tempor	tempor	escule	tempor	pipien	phyllomedus	rana escule	phyllomedus	agalychnis	cia cae	kassina sen	phyllomedus	litoria cae	agalychnis	agalychnis	phyllomedus	pachymedusa	phyllomedus	agalychnis	phyllomedus
tion	rana	rana	rana	rana	rana	rana	rana	rana	rana	rana	phy]]	rana	phy11	agaly	litor	kassi	phyll	litor	agaly	agaly	phy11	pachy	phy11	agaly	phyll						
Description	P79875	P79874	P79876	P39084	P32412	P80399	08qfq5	Q7£2v5	P80398	Q8qfq4	090wp7	P82268	P82269	P40842	P83719	Q8qfq3	Q800r3	P40844	Q800£1	080082	Q800r8	Q90w78	P81488			093225	090zk3		9	~ #	Q7t3k6
																							•								
SUMMAKIES	TEMG RANTE	TEMB RANTE	TEMH_RANTE	RLXN RANCA	BR1E RANES	GGNS_RANRU	BR1B_RANPI	Q7T2V5	GGN4 RANRU	RN2P RANPI	PLR RANPI	BRTA RANTE	BRTB RANTE	BR2F RANES	RAYT RANTE	RN2A RANPI	Q800R3	ES1B RANES	Q800F1	Q800S2	Q800R8	GALE_KASSE	DRG3_PHYBI	Q800R9	080080	DMS5_AGAAN	DRG1_PHYBI	DEM PACDA	DMS4_PHYBI	DMS4_AGAAN	Q7T3K6
ОВ	-		н	Н	Н	-	-	~	-	ч	Н	-	-	-	-	-	~		~	7	~	-	-	~	N	П	~1		-		~
% Query Match Length	61	61	58	99	17	65	69	331	80	71	62	74	74	74	62	70	99	84	62	71	75	72	77	75	75	72	81	201	16	72	79
% Query Match	100.0					61.9	60.3	50.7	48.4	47.4	47.1	45.3	45.3	44.9	44.4	44.1	43.5	39.5	38.1	36.3	35.9	35.6	35.6	35.3	35.0	34.8	34.6	34.6	34.5	34.3	34.3
Score	306	245	219.5	212	211.5	189.5	184.5	155	148	145	144	138.5	138.5	137.5	136	135	133	120	116.5	111	110	109	109	108	107	106.5	106	106	105.5	105	105
Regult No.	-	7	m	4	S	9	7	80	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31

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Query Match
100.0%; Score 306; DB 1; Length 61;
Best Local Similarity 100.0%; Pred. No. 3.8e-25;
Matches 61; Conservative 0; Mismatches 0; Indels

Q7t3k7 phyllomedus	i d	93222 agalychnis	7113k8 phyllomedus	800s1 agalychnis	93452 pachymedusa	90zk5 phyllomedus	80282 phyllomedus	93226 agalychnis	31107 phyllomedus	81490 phyllomedus	phyl	800r6 litoria cae
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eur. J. Biochem. 242:788-792(1996).

- I- FUNCTION: Has no antibacterial activity.

- I- SUBCELLULAR LOCATION: Secreted.

- I- SIMILARITY: Stin.

- I SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.

Brevinin subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MFTLKKSLLLLFFLGTINLSLCEEERDADEERRDDLEERDVEVEKRFFPVIGRILNGILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUENCE FROM N.A., AND SEQUENCE OF 47-66.
TISSUE-Skin, and Skin secretion;
MEDLINE=94193722; PubMed=8144672;
Clark D.P., Durell S., Maloy W.L., Zasloff M.;
"Ranalexin. A novel antimicrobial peptide from bullfrog (Rana catesbeiana) skin, structurally related to the bacterial antiblotic,
                                                                                                                                                                                                                                       "Temporins, antimicrobial peptides from the European red frog Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rana catesbeiana (Bull frog).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                     Rana temporaria (Buropean common frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF03032; Brevenin; 1.
Amidation; Amphibian defense peptide; Direct protein sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leucine amide (G-57 provides amide
                                                                                                                                       SEQUENCE OF 47-56, AND SYNTHESIS OF 47-56
                                                                                                                                                                                               Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 219.5; DB 1; Length
Pred. No. 5.8e-16;
7; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          group).
684AECB0451E5E81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 AA.
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                                                                                                                                         SEQUENCE FROM N.A., SEQUENCE OF 4
TISSUE=Skin, and Skin secretion;
MEDLINE=97175050; PubMed=9022710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Y09394; CAA70563.1; -.
InterPro; IPR004275; Brevenin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 73.8%;
Matches 45; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=8400;
                                                                                               NCBI_TaxID=8407;
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                                                                                                                                                                                                                                                                  temporaria.";
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P39084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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PEPTIDE
MOD_RES
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RLXN_RANCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUB SPECIFICITY: Skin.
-!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
Brevinin subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MFTLKKSLLLLFFLGTINLSLCEEERDADEERRDDLEERDVEVEKRFFPVIGRILNGILG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Temporins, antimicrobial peptides from the Buropean red frog Rana
                                                                                                                                                                                                                                                                                     Rana temporaria (European common frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
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Leucine amide (G-60 provides amide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biochem. 242:788-792(1996). FUNCTION: Has antibacterial activity against Gram-positive
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., SEQUENCE OF 47-59, AND SYNTHESIS OF 47-59. TISSUE=Skin, and Skin secretion;
MEDLINE=97175050; PubMed=9022710;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 245, DB 1; Length 61;
Pred. No. 1.2e-18;
9; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        group).
B73F75689C300357 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amidation; Amphibian defense peptide; Antibiotic;
                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TEMH_RANTE STANDARD; PRT; 58 AA. 1D TEMH RANTE STANDARD; PRT; 58 AA. AC P79876; P55922; DT 01-NOV-1997 (Rel. 35, Created) DT 01-NOV-1997 (Rel. 35, Last sequence update)
                                                                                                                                                                    61 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR004275; Brevenin.
Pfam; PF03032; Brevenin; 1.
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                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                      Temporin B precursor
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Matches

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RESULT 3

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TISSUE-Skin secretion;
MEDLINE-93285327; PubMed-8508915; DOI-10.1016/0014-5793(93)81384-C;
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45
71
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Park J.M., Lee J.Y.,
Submitted (MAY-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; C53578; C53578.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 AA;
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Best Local (
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GGN5_RANRU
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                           셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MFTLKKSLLLLFFLGTINLSLCEEERDADEERRDDLEERDVEVEKRFFPVIGRILNGIL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MFTLKKSLLLLFFLGTINLSLCEBERNABEERRDNPDERDVEVEKRFLGGLIKIVPAMI 59
                                                                                                                                                                                                           peptide ranalexin and a study

Eur. J. Blochem. 253:221-228(1998).
-!- FUNCTION: Potent microbicidal activity, active against S.aureus and B.coli. It acts as well as a membrane-disruptive agent at higher concentrations.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
-!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
-!- Grantle STAGE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps .
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
                                                                                                                          MEDLINE=98237592; PubMed=9578480;
Vignal E., Chavanieu A., Roch P., Chiche L., Grassy G., Calas B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam, PF03032; Brevenin; 1.
Amphibian defense peptide; Antibiotic; Direct protein sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Simmaco M., Mignogna G., Barra D., Bossa F.; Mathindrobial peptides from shin secretions of Rana esculenta. Molecular cloning of cDNAs encoding esculentin and brevinins and isolation of new active peptides.";
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                                                                                                                                                                                                                                    its interaction with perdeuterated dodecylphosphocholine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              096B8AD58A3C8513 CRC64;
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Small acidic peptide
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                           "Solution structure of the antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ranalexin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 48-71, AND DISULFIDE BOND
                                                  Biol. Chem. 269:10849-10855(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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01-FEB-1995 (Rel. 31, Last seqn
05-JUL-2004 (Rel. 44, Last anno
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                                                                           [2]
STRUCTURE BY NMR OF RANALEXIN
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7615 MW;
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les 43; Conservative
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polymyxin.";
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P32412;
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RC TISSUE
RC AMPLIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MFTLKKSMILLFFLGTINLSLCEEERDADEEERRDNPDESEVEVEKRFLPLLAGIAANFL 60
                                                               Rana esculenta.";
PRBS Lett. 324:159-161(1993).
-!- FUNCTION: Shows antibacterial activity against representative
Gram-negative and Gram-positive bacterial species, and a very high
Simmaco M., Mignogna G., Barra D., Bossa F.; "Novel antimicrobial peptides from skin secretion of the European frog
                                                                                                                                                                                                    hemolytic activity.
--- SUBCELLULAR LOCATION: Secreted.
--- TISSUE SPECIFICITY: Skin.
--- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
--- Brevinin subfamily.
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Park W., Jung J.-E., Lee B.J.;
"Antimicrobial peptides from the skin of a Korean frog, Rana rugosa.";
Blochem. Biophys. Res. Commun. 205:948-954(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MFTLKKSLLLLFFLGTINLSLCBERDAD-BERRDDLBERDVBVEKRFFPVIGRILNGIL
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Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF03032; Brevenin; 1.
Amphibian defense peptide; Antibiotic; Direct protein sequencing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moon H.M., Lee B.J.;
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L -> F (in brevinin-1EC)
10900AC2BC71BB73 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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8267 MW;
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llarity 71.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22830827; PubMed=12948838; DOI=10.1016/S0196-9781(03)00166-9; MEDLINE=22830827; PubMed=12948838; DOI=10.1016/S0196-9781(03)00166-9; Li L., Bjoureon A.J., He J., Cai G., Rao P., Shaw C.; Bradykining and their cDNA from piebald odorous frog, Odorrana schmackeri, extin.; Peptides 24.863-872(2003).

EMBL; AJ544062; CAD66432.1; -. CGO; GO:0005276; C:extracellular; IEA.

GO; GO:0004742; P:edfense response to bacteria; IEA.

InterPro; IPR04725; Brevenin.
                    SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
                                                                                                                                                                                                                                         Interpro; IPR004275; Brevenin.
Pfam; PF03032; Brevenin; 1.
Amphibian defense peptide; Antibiotic; Direct protein sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 69;
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D7DF35CB3A45066D CRC64;
                                                                                                                                                                                                                                                                                                                                                                      By similarity.
31B16331997DC170 CRC64;
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Pred. No. 3.7e-12;
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                                                                                                                                                                                                                            EMBL; AJ427746; CAD20745.1; -.
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7929 MW;
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63
69 AA;
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SEQUENCE
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                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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Bur. J. Blochem. 267:884-900(2000)
Fur. J. ROCTION: Antibacterial activity against Gram-positive bacterium
S.aureus and Gram-negative bacterium E.coli. Has activity against
                                                              -i- SUBÜNIT: Monomer.
-i- SUBCELLÜLAR LOCATION: Secreted.
-i- TISSUB SPECIFICITY: Skin.
-i- TISSUB SPECIFICITY: Belongs to the frog skin active peptide (FSAP) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
FUNCTION: Has a non-hemolytic activity. Has a broad spectrum of activity against both Gram-positive and Gram-negative bacteria, fungi and protozoa.
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TISSUE SPECIFICITY: Skin.
MASS SPECTROMETRY: MW=2577.1; METHOD=Electrospray; RANGE=46-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brevinin-1Pb precursor.
Rana pipiens (Northern leopard frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Skin secretion;
Bibline=20117700; PubMed=10651828;
Goraya J., Wang Y., Li Z., O'Flaherty M., Knoop F.C., Platz J.E.,
Conlon J.M.;
                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR004275; Brevenin.
Pfam, PP03032; Brevenin; 1.
Amphibian defense peptide; Antibiotic; Direct protein sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 189.5; DB 1; Length 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cloning of Rana pipiens skin peptides.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  By Similarity.
F -> K (in Ref. 2).
312480B6E67D4845 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 46-69, FUNCTION, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1e-12;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8QFG5; P82842;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
05-UUJ-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaegurin-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IISSUE=Skin;
Farragher S.M., Bjourson A.J., Shaw C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Potential.
                                                                                                                                                                                                                                                                                                                   EMBL; U22393; AAA64412.1; -. PIR; S59962; S59962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.8$;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7414 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                    Brevinin subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                 22
33
65
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58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=8404;
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                  Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEPTIDE
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Length 331,

Gape

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14; Indels

Length 80;

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Query Match
Best Local Similarity 49.33
Matches · 34; Conservative
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RN2P RANPI
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             ä
                                                                                                                                                                                                                                                                                                                                                                                                                                         Park J.M., Jung J.-E., Lee B.J.,
"Antimicrobial peptides from the skin of a Korean frog, Rana rugosa.";
"Antimicrobial peptides from the skin of a Biochem. Biophys. Res. Commun. 205:948-954(1994).

-IONCTION: Has a non-hemolytic activity. Has a broad spectrum of activity against both Gram-positive and Gram-negative bacteria,
                                                                                                                                                                                                                                                                                                                                     MEDLINE=20461174; PubMed=11004488; DOI=10.1016/S0167-4781(00)00082-8; Kwon S.Y., Carlson B.A., Park J.M., Lee B.J.; "Structural organization and expression of the gaegurin 4 gene of Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBŪNIT: Monomer.
SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Skin.
SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
             Gaps
                                                                                                                                                                                     Rana rugosa (Wrinkled frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amphibian defense peptide; Antibiotic; Direct protein sequencing;
             4;
             3; Indels
                                  44
                                              MFTLKKSLILLFFLGTINLSLCKQERDADE----DENEREAKVE 40
                                                                                                                                                                                                                                                                             Moon H.M., Lee B.J.;
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaegurin-4.
By similarity.
Missing (in Ref. 2).
K -> L (in Ref. 3).
D79FC76D2995F4B6 CRC64;
                                1 MFTLKKSLLLLFFLGTINLSLCEEERDADEERRDDLEERDVEVE
Pred. No. 2.4e-08;
                                                                                                             GGN4 RANRU STANDARD; PRT; 80 AA. P80398; Q9128; Q98TA6; 01-NOV-1995 (Rel. 32, Created) 05-ULV-1997 (Rel. 35, Last sequence update) 05-ULL-2004 (Rel. 44, Last annotation update) Gaegurin-4 precursor.
             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   Biochim. Biophys. Acta 1492:185-190(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95091844; PubMed=7999137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S59961; S59961.
InterPro; IPR004275; Brevenin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF213015; AAK26444.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U22392; AAA64411.1; -.
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW.
             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF03032; Brevenin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22
41
80
80
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78
8695 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fungi and protozoa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brevinin subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Skin secretion;
                                                                                                                                                                                                                                                                             Park J.M., Lee J.Y.,
Submitted (MAY-1995)
Best Local Similarity
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 44-80.
                                                                                                                                                                                                                                                                   rissum-skin;
                                                                                                                                                                                                                                                                                                                              TISSUE=Skin
                                                                                                                                                                                   Name=GGN4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULPID
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                           rugosa."
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                                                                                                     RANRU
             Matches
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                    22
                                                                                                                                                   1 MFTWKKSLLFLFFLGTISLSLCEEERSADEDDGGEWTEEEVKGILDTLKQFAKGVGKDL 60
                                                                                                                    1 MFTLKKSLLLLFFLGTINLSLCEEERDADEERRDDLEERDV----EVEKRFFPVIGRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Peptides with antimicrobial activity from four different families isolated from the skins of the North American frogs Rana luteiventris, Rana berlandieri and Rana pipiens."; Eur. J. Biochem. 267:894-900(2000).

    -!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Antibacterial activity against Gram-positive bacterium S.aureus and Gram-negative bacterium E.coli. Has activity against
                                                                Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBCELLULAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: Skin.
-1- MASS SPECIFOMETRY: MW=3000.1; METHOD=Blectrospray; RANGE=45-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ranatuerin-2P precursor.
Rana pipiens (Northern leopard frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUB-Skin secretion;
MEDLINE-20117700; PubMed=10651828;
Goraya J., Wang Y., Li Z., O'Flaherty M., Knoop F.C., Platz J.E.,
Conlon J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF03032; Brevenin; 1.
Amphibian defense peptide; Antibiotic; Direct protein sequencing;
                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;;
7
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                                                          14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Farragher S.M., Bjourson A.J., Shaw C.;
"Cloning of Rana pipiens skin peptides.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    By similarity.
C871C47FC27FFDEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 45-71, FUNCTION, AND MASS SPECTROMETRY
%; Score 148; DB 1;
%; Pred. No. 3.3e-08;
11; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8QFQ4; P82847;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1- FUNCTION: Antibacterial activity against
                                                                                                                                                                                                                                                                                                                                                                                                                                                71 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ranatuerin-2P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR004275; Brevenin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ427747; CAD20746.1; -.
   48.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brevinin subfamily
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                                                                                                                                                                                                                                                                                                VKGAAQGVL 69
                                                                                                                                                                                                                                     26 ----NGIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=8404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE=Ref.2.
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Best Local Simi
Matches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                RN2P RANPI
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                                      MFTLKKSLLLLFFLGTINLSLCEEERDADEERRDDLEERDVEVEKRFFPVIGRILNGILG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochemistry 42:14023-14035(2003).

-I FUNCTION: Mast cell degranulating peptide. Antiproliferative activity against human breast and ovarian tumor cell lines in vitro. Inhibits granulopoiesis in rat in vitro. Causes histamine release from rat peritoneal mast cells in vitro. Has antibacterial activity against Gram-positive bacteria B imegaterium Bml1, S.lentus and M.luteus, and antifungal activity against Ctropicalis, C. guiller-mondil and P. nicotianas spores. Has hemolytic activity. The mature peptide inserts into the hydrophopic core of the bacterial cell membrane and increases permeability without disrupting membrane integrity. Probably binds to the outer membrane surface before aggregating to form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bienert M., Shaw Č.,
"Peptide leucine arginine, a potent immunomodulatory peptide, isolated
and structurally characterized from the skin of the Northern Leopard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECTROMETRY: MW=2136; METHOD=Plasma desorption; RANGE=44-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Ranacyclins, a new family of short cyclic antimicrobial peptides:
biological function, mode of action and parameters involved in target
specificity.";
                                                                                                                                                                                                                                                                                                                                                                    Farragher S., Bjourson A.J., McClean S., Orr D.F., Shaw C.; "Cloning of CDNAs encoding defensive skin secretion peptides from the Northern leopard frog (Rana pipiens)."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Venom;
MEDLINE=98338373; PubMed=9673585;
Boyer M., van Den Berg H.W., Shaw C., Lynch M., Johnston P.;
"Breast cancer cell lines express specific binding sites for plr, a
novel anti-proliferative peptide from frog skin venom.";
Br. J. Cancer 78:41-41(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 44-61, FUNCTION, MASS SPECTROMETRY, DISULPIDE BOND, CIRCULAR DICHROISM ANALYSIS, SYNTHESIS, AND 3D-STRUCTURE MODELING.
                                                                                                                                                                                                                                               Rana pipiens (Northern leopard frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mangoni M.L., Papo N., Mignogna G., Andreu D., Shai Y., Barra D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Skin secretion;
MEDLINE=21167822; PubMed=11099505; DOI=10.1074/jbc.M009680200;
Salmon A.L., Cross L.J.M., Irvine A.E., Lappin T.R.J., Dathe M. Krause G., Canning P., Thim L., Beyermann M., Rothemund S.,
                                                                                                                                                                                          10-OCT-2003 (Rel. 42, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Peptide leucine arginine precursor (pLR).
                                                                                                                                            Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=14636071; DOI=10.1021/bi0345211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol. Chem. 276:10145-10152(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Secreted.
                                                                                                                                         PLR RANPI STANDARD; E 090WP7; P81110; I 10-0CT-2003 (Rel. 42, Last sequence-2004 (Rel. 44, Last sequence-2004 (Rel. 44, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY: Skin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brevinin subfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rana pipiens."
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                    NCBI_TaxID=8404;
                                                                                                                                                                                                                                                                                                                                                        rissue=Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Simmaco M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             frog,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SUBCELLULAR LOCATION: Secreted.
-i- TISSUE SPECIFICITY: Skin.
-i- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cleavage on pair of basic residues; Direct protein sequencing;
Fungicide; Hemolysis; Inflammatory response; Mast cell degranulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MFTLKKSLLLLFFLGTINLSLCEERDADEERRDDLEERDVEVEKRFFPVIGRILNG
                                                                                                                                                              GO; GO:0005576; C:extracellular; IDA.
GO; GO:0050832; P:defense response to fungi; IDA.
GO; GO:0050830; P:defense response to Gram-positive bacteria; IDA.
InterPro; IPR004275; Brevenin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Amphibia, Batrachia, Anura, Neobatrachia, Ranoldea, Ranidae, Rana
                                                                                                                                                                                                                                                                                                                                                                                                                 Arginine amide (G-62 provides amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR004275; Brevenin.
Pfam; PF03032; Brevenin; 1.
Amphibian defense peptide; Antibiotic; Hemolysis; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Indels
                                                                                                                                                                                                                                                                                                                                                                              Peptide leucine arginine
                                                                                                                                                                                                                                                                                                                                                                                                                                           group).
C8F7F58849A01A1C CRC64;
                                                                                                                                                                                                                                               Pfam; PF03032; Brevenin; 1.
Amidation; Amphibian defense peptide; Antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 144; DB 1;
; Pred. No. 6.8e-08;
11; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brevinin-2Ta precursor.
Rana temporaria (European common frog).
                                                                                                                                                                                                                                                                                                                                             Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ251567; CAB61442.1; -.
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                                                                                                                                                      EMBL; AJ414584; CAC93861.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         7113 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30; Conservative
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                                                                                                                                                                                                                                                                                                                                             20
41
61
58
61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BRTA RANTE
                                                                                                                                                                                                                                                                                                                                                                              PEPTIDE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                           Signal.
                                                                                                                                                                                                                                                                                                                                               SIGNAL
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BRTA RANTE
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Matches

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5543

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SÜBCELLÜLAR LOCATION: Secreted.
-1- TISSUB SPECIFICITY: Skin.
-1- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
Brevinin subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 269:11956-11961(1994).
-1- FUNCTION: Shows antibacterial activity against representative Gram-negative and Gram-positive bacterial species, and hemolytic
                                                                                                          Rana esculenta (Edible frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amplibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
NCR1, marth-R407.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rana temporaria (European common frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                    Simmaco M., Mignogna G., Barra D., Bossa F.;
Antimicrobial peptides from skin secretions of Rana esculenta.
Molecular cloning of CDNAs encoding esculentin and brevinins and
isolation of new active peptides.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mangoni M.L., Papo N., Mignogna G., Andreu D., Shai Y., Barra D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amphibian defense peptide; Antibiotic; Hemolysis; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MFTLKKSLLLLFFLGTINLSLCEEERDADEERRDDLEERDVEVEKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1] ... SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 By similarity.
48044D3F01E6D78D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 137.5; DB 1;
Pred. No. 4e-07;
  01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brevinin-2Ef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=14636071; DOI=10.1021/bi0345211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                          MEDLINE=94216303; PubMed=8163497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR004275; Brevenin.
Pfam; PF03032; Brevenin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                             Brevinin-2Ef precursor.
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                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 AA;
                                                                                                                                                                                                   NCBI_TaxID=8401;
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P83719;
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     셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- FUNCTION: Shows antibacterial activity against representative Gram-negative and Gram-positive bacterial species (By similarity).
-i- SHECELLULAR LOCATION: Secreted.
-i- TISSUE SPECIFICITY: Skin.
-i- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family. Brevinin subfamily.
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Simmaco M., Mignogna G., Barra D.;
"Antimicrobial peptides from amphibian skin: what do they tell us?";
Biopolymers 47:435-450(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rana temporaria (European common frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
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Pfam; PF03032; Brevenin; 1.
Amphibian defense peptide; Antibiotic; Direct protein sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF 42-74.
TISSUES-Skin, and Skin secretion;
MEDLINE=92266278; Pubmed=10333336,
DOI=10.1002/(SICI)1097-0282(1998)47:6<435::AID-BIF3>3.3.CO;2-#;
                                                                                                                                                                                             5,
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                                                                                                                                    Score 138.5; DB 1; Length 74;
Pred. No. 3.1e-07;
6; Mismatches 5; Indels
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                                                                                                                                                                                                                                                    46
                                                                                                                                                                                                                                                                           1 MFTMKKSLLLFFFLGTISLSLCQEERNADEDDGEMTEE----EKR 41
                                                                                                                                                                                                                                                 1 MFTLKKSLLLLFFLGTINLSLCEEERDADEERRDDLEERDVEVEKR
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                                                      By similarity.
55E0FDF790B78F75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             By similarity.
5B26718D62B79387 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 40, Last sequence update) (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                              74 AA
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                               Brevinin-2Ta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AJ251566; CAB61445.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 40, Created)
                                                                                                                                 45.3%;
illarity 65.2%;
Conservative 6
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23 39
42 74
68 74
74 AA; 8193 MW;
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                                                   74
8162 MW;
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Best Local Similarity 65.2
Matches 30, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brevinin-2Tb precursor.
                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hemolysis; Signal.
                                                                             74 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=8407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001
                                                                                                                                                                                          30;
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BR2F_RANES
ID BR2F_RANES
AC P40842;
                                                                                                                                                                                                                                                                                                                                                                                                               BRTB_RANTE
ID BRTB_RANTE
AC P82269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004
                                                DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
PROPEP
PEPTIDE
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Gaps

2

Indels

4;

46

SIGNAL

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Length 74;

"Ranacyclins, a new family of short cyclic antimicrobial peptides:

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                       form transmembrane pores.
SUBCELLULAR LOCATION: Secreted (By similarity).
TISSUE SPECIFICITY: Expressed by the skin granular glands.
SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
Brevinin subfamily.
biological function, mode of action and parameters involved in target appecificity.";
Blochemistry 42:14023-14035(2003).

- FUNCTION: Has antibacterial activity against Gram-positive bacteria B.megaterium Bml1, S.lentus and M.luteus, and Gram-negative bacteria B.coli D22, Y.pseudotuberculosis YP III and P.Syringae pv tabaci, and antifungal activity against C.albicans ATCC 10231, C.tropicalis, C.guiller-mondii and P.nicotiane sporces .Has weak hemolytic activity. The mature peptide inserts into the hydrophobic core of the bacterial cell membrane and increases permeability without disrupting membrane integrity.

Probably binds to the outer membrane surface before aggregating t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             By similarity.
Lysine amide (G-61 provides amide group)
55A4283837A11E82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ583866; CAE48162.1; -.
InterPro; IPR004275; Brevenin.
Amidation; Amphibian defense peptide; Antibiotic;
Cleavage on pair of basic residues; Fungicide; Hemolysis; Signal.
SIGNAL
1 2 Potential.
PROPEP 23 43 Potential.
CHAIN 44 60 Ranacyclin T.
DISULFID 49 59 Similarity.
MOD RES 60 60 Lysine amide (G-61 provides amide gr SEQÜENCE 62 AA; 6983 MW; 55A4283837A11E82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                This SWIS
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Search completed: March 30, 2005, 17:29:54 Job time : 184 secs

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Gaps

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Score 136; DB 1; Length 62; Pred. No. 4.8e-07; 9; Mismatches 7; Indels

Pred. No. 4.8e 9; Mismatches

44.4%; ilarity 61.9%; Conservative

Local Similarity es 26; Conserv

Query Match

- protein search, using sw model OM protein March 30, 2005, 17:20:45; Search time 43 Seconds Run on:

(without alignments) 136.494 Million cell updates/sec

US-10-719-623A-16

score:

306 1 MFTLKKSLLLLPFLGTINLS.......EVEKRFFPVIGRILNGILGK Sequence:

61

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

hypothetical prote hypothetical prote hypothetical prote procaerulein prote procaerulein prote brevinin-2Ef precu esculentin-1b prec dermaseptin b I pr adenoregulin precu dermaseptine B3 pr dermorphin precurs [D-Ala(2)] deltorp protein disulfideamyloid beta (A4) hypothetical prote protein F26H11.1 [ranalexin precurso antimicrobial pept antimicrobial pept hypothetical prote caerulein precurso hypothetical prote efflux protein, [im hypothetical prote Cytochrome P450 71 Description SUMMARIES JN04662 110456 A27784 A237784 A23726 A23726 G69850 G69850 G69850 G70428 A73364 A73263 A732373 S59961 B53578 A53578 B54897 A53744 C53578 S59962 8 Length Query Score 211.5 189.5 148 137.5 120 103 103 99.5 98.5 70.5 70 69.5 69 Result

probable ubiquitin	hypothetical prote	hypothetical prote	NF-180 - sea lampr	hypothetical prote	hypothetical prote	hypothetical prote	conserved hypothet	hypothetical prote	hypothetical prote	hypothetical prote	glutamic acid-rich	hypothetical prote	3-isopropylmalate	hypothetical prote	nucleophosmin NO38
T51964	T21434	G96513	151116	529796	S29795	D96723	G70234	T48398	F75070	D69152	A54514	T21910	A72363	F84798	A41730
7	~	~	7	N	N	~	~	7	0	N	N	N	~	~	N
241	244	316	1110	630	721	1198	172	81	150	289	678	1430	166	232	296
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20	20	20	20	20.1	20	13	13	13	13	19	13	13	13	13	19
62	62	62	62	61.5	61.5	61	60.5	9	9	9	9	9	59.5	59.5	59.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

```
A;Accession: A53744
A;Status: preliminary; not compared with conceptual translation
A;Nolecule 'type: mBNA
A;Residues: 1-66 <CLA>
A;Cross-references: UNIPROT:P39084; GB:S69903; NID:g546211; PIDN:AAB30394.1; PID:g546212
C;Superfamily: ranalexin precursor; dermorphin precursor amino-terminal homology
C;Keywords: disulfide bond; skin
F;1-46/Domain: dermorphin precursor amino-terminal homology <DER>
F;47-66/Product: ranalexin #status experimental <MAT>
F;60-66/Disulfide bonds: #status experimental
                                                                                                                                                                                                         (Rana catesbeiana) skin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ranalexin precursor - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Accession: A53744
R;Clark, D.P.; Durell, S.; Maloy, W.L.; Zasloff, M.
J. Biol. Chem. 269, 10849-10855, 1994
A;Title: Ranalexin. A novel antimicrobial peptide from bullfrog (Rana catesb A;Reference number: A53744; MUID:94193792; PMID:8144672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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RESULT 2

Drevinin-1Ec precursor - edible frog
brevinin-1Ec precursor - edible frog

NyAlternate names: antimicrobial peptide brevinin 1B
C;Species: Rana esculenta (edible prog)
C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 09-Jul-2004
C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 09-Jul-2004
C;Date: 12-Apr-1995 #sequence_revision 15-Apr-1995 #text_change 09-Jul-2004
C;Date: 12-Apr-1995 #sequence_revision 0; Bossa, F.
A;Simmaco, M.; Mignogna, G.; Barra, D.; Bossa, F.
A;Residues: 1-71 <SIM
A;Residues: 1-71 <SIM
A;Residues: 1-71 <SIM
A;Residues: 1-71 *SIM
A;Reference number: S33729; MUD:93285327; PMID:8508915
A;Title: Novel antimicrobial peptides from skin secretion of the European frog Rana escul
A;Residues: 24-71 <SIM
A;Residues: 48-71 <SIM
A;Residues: 48-71 <SIM
A;Residues: 48-71 <SIM

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A;Title: Molecular cloning of cDNAB encoding precursors of frog skin antimicrobial peptic A;Reference number: S59961; MUID:96038814; PMID:7578251 A;Accession: S59961
                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-80 < PAR>
Biochem. Biophys. Res. Commun. 205, 948-954, 1994
A; Ritle: Antimicrobial peptides from the skin of a Korean frog, Rana rugosa.
A; Reference number: PC2303
A; Reference number: PC2303
A; Reference number: PC2303
A; Reference number: PC2303
A; Molecule type: protein
A; Reference number: PC2303
A; Molecule type: protein
A; Reference number: PC303
A; Molecule type: protein
A; Reparamental source: skin
C; Comment: This peptide has antimicrobial activity.
C; Reywords: antibacterial; antibiotic; antifungal; disulfide bond; skin
F; 1-43/Domain: dermorphin precursor amino-terminal homology C; Reywords: antibacterial; antibiotic; antifungal; disulfide bond; skin
F; 1-43/Domain: propeptide #status predicted < SIG>
F; 21-34/Domain: propeptide #status predicted < SIG>
F; 74-80/Product: antimicrobial peptide gaegurin 4 #status experimental < MAT>
F; 74-80/Region: rana box motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MFTLKKSLLLLFFLGTINLSLCEBERDADEERRDDLEERDV----EVEKRFFPVIGRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.4%; Score 148; DB 2; 49.3%; Pred. No. 2.1e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 ---- NGIL 59
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A/Experimental source: skin
R/Experimental source: skin
R/Experimental source: skin
Biochem. Biophys. Res. Commun. 205, 948-954, 1994
A/Title: Antimicrobial peptides from the skin of a Korean frog, Rana rugosa.
A/Reference number: PC2300; MUID:95091844; PMID:7999137
A/Recession: PC2304
A/MOlecule type: protein
A/Residues: 42-57, KY, 59-65 < PAW>
A/Residues: 42-65 < PAW>
A/Residues:
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C;Species: Rana rugosa (Korean frog)
C;Species: Rana rugosa (Korean frog)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S59962; PC2304
R;Park, J.M.; Lee, J.Y.; Moon, H.M.; Lee, B.J.
Blochim: Blophys. Acta 1264, 23-25, 1995
A;Attle: Molecular cloning of cDNAs encoding precursors of frog skin antimicrobial peptials A;Reference number: S59961; MUID:96038814; PMID:7578251
A;Accession: S59962
                      A, Experimental source: skin
C, Function:
A, Description: has antimicrobial and hemolytic activity
C, Superfamilion: has antimicrobial and hemolytic activity
C, Superfamily: ranalexin precursor, dermorphin precursor amino-terminal homology
C, Keywords: antibacterial; disulfide bond; hemolysis; skin
F;1-27/Domain: dermorphin precursor amino-terminal homology <DER>F;1-27/Domain: signal sequence #status predicted <SIG>F;3-47/Domain: propeptide #status predicted <PRO>F;3-47/Domain: broyphin-1Ec #status experimental <MAT>F;65-71/Disulfide bonds: #status predicted
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C;Species: Rana rugosa (Korean frog)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S59961; PC2303
R;Park, J.M.; Lee, J.Y.; Moon, H.M.; Lee, B.J.
Biochim. Biophys. Acta 1264, 23-25, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MPTLKKSMLLLEPLGTINLSLCEBERDADEBERRDNPDESEVEVEKRFLPLLAGLAANFL
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Pred. No. 4.6e-14;
8; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.1%; Sco... 71.0%; Pred. No. 1.... 7; Mismatches
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Best Local Similarity 67.8%;
Matches 40; Conservative 6
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A; Residues: 1-65 < PAR>
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Clacesion: B35578
R/Simmaco, M.; Mignogna, G.; Barra, D.; Bossa, F.
J. Balol. Chem. 269, 11956-11861, 1994
A.Title: Antimicrobial peptides from 8tin secretions of Rana esculenta. Molecular cloning A.Title: Antimicrobial peptides from 8tin secretions of Rana esculenta. Molecular cloning A.Facession: B53578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ã
esculentin-1b precursor - edible frog
C;Species: Rana esculenta (edible frog)
C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 09-Jul-2004
C;Accession: A53578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      brevinin-2Ef precursor - edible frog
C;Species: Rana esculenta (edible frog)
C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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dermorphin precursor 2 - Sauvage's leaf frog (fragment)
N;Contains: dermorphin
C;Species: Phyllomedusa sauvagei (Sauvage's leaf frog)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C;Accession: B27784
R;Richter, K.; Egger, R.; Kreil, G.
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Best Local Similarity 45.8<sup>1</sup>
Matches 22; Conservative
                                                       A; Residues: 1-81 <AMI>
                                                                                                                                                                                                                                                                                                                                                                       A, Accession: A54897
A, Molecule type: mRNA
A, Residues: 1-81 <AM2>
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Risimmaco, M.; Mignogna, G.; Barra, D.; Bossa, F.
J. Biol. Chem. 269, 11956-11961, 1994
A; Title: Antimicrobial peptides from skin secretions of Rana esculenta. Molecular clonin A; Reference number: A53578; MUID:94216303; PMID:8163497
A; Accession: A53578
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-84 <SIM>A; Cross-references: UNIPROT:P40844; GB:X77833; NID:9488374; PIDN:CAA54844.1; PID:9140579
C; Superfamily: ranalexin precursor; dermorphin precursor amino-terminal homology
C; Superfamily: ranalexin precursor amino-terminal homology
C; Superfamily: ranalexin precursor amino-terminal homology
F; 1-38/Domain: dermorphin precursor amino-terminal homology
F; 1-22/Domain: signal sequence #status predicted <SIG>F; 23-38/Domain: signal sequence #status predicted <PRO>F; 39-84/Product: esculentin-1b #status predicted <MAT>F; 78-84/Disulfide bonds: #status predicted <MAT>F; 78-84/Disulfide bonds: #status predicted
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C;Species: Phyllomedusa bicolor (two-colored leaf frog)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C;Accession: B54897
C;Accession: B54897
R;Amiche, M.; Ducancel, F.; Mor, A.; Boulain, J.C.; Menez, A.; Nicolas, P.
J. Biol. Chem. 269, 17847-17852, 1994
A;Title: Precursors of vertebrate peptide antibiotics dermaseptin b and adenoregulin hav
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C; Accession: JN0462; A54897; A44171; S34718
R; Amiche, M.; Ducancel, F.; Lajeunesse, E.; Boulain, J.C.; Menez, A.; Nicolas, P.
Biochem. Biophys. Res. Commun. 191, 983-990, 1993
A; Title: Molecular cloning of a cDNA encoding the precursor of adenoregulin from frog A; Reference number: JN0462; MJID:93221546; PMID:8466537
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Pred. No. 2.6e-06;
9; Mismatches 13; Indels
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JN0462.
JN0462.
Abdooregulin precursor - two-colored leaf frog
N,Alternate names: dermaseptin b II
C,Species: Phyllomedusa bicolor (two-colored leaf frog)
C,Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text
C,Accession: JN0462, A54897, A44171; S34718
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Best Local Similarity 47.5-
Best Local Similarity 27.5-
Conservative
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A;Molecule type: mRNA
A;Residues: 1-78 <AMI>
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A; Cross-references: UNIPROT: P31107; EMBL: X70278; NID: 9395931; PIDN: CAA49763.1; PID: 939593. A; Experimental source: skin A; Note: the authors translated the codon AAA for residue 26 as Leu A; Note: the authors translated the codon AAA for residue 26 as Leu B; Amoriche, M.; Ducancel, F.; Mor, A.; Boulain, J.C.; Menez, A.; Nicolas, P. J. Biol. Chem. 269, 17847-17852, 1994 A; Title: Precursors of vertebrate peptide antibiotics dermaseptin b and adenoregulin hav:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Cross-references: GB:X70278; NID:g395931; PIDN:CAA49763.1; PID:g395932
R;DBly, J.W.; Caceres, J.; Moni, R.W.; Gusovsky, F.; Moos Jr., M.; Seamon, K.B.; Milton, Proc. Natl. Acad. Sci. U.S.A. 89, 10960-10963, 1992
A;Title: Frog secretions and hunting magic in the upper Amazon: identification of a pept A;Reference number: A44171; MUID:93066363; PMID:1438301
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J. Biol. Chem. 273, 14690-14697, 1998
J. Fitle: Structure, synthesis, and molecular cloning of dermaseptins B, a family of skin A; Reference number: 217027; WUID:98278974; PMID:9614066
A; Accession: T10456
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A;Nolecule rype: manA
A;Residues: 1-74 < CCHA>
A;Residues: 1-74 < CCHA>
A;Residues: 1-74 < CCHA>
A;Cross-references: UNIPROT:P81485; EMBL:Y16564; NID:g3256036; PIDN:CAA76288.1; PID:g3256
C;Suporfamily: dermaseptin precursor; dermorphin precursor amino-terminal homology
F;1-22-Domain: signal sequence #status predicted <SIG>
F;23-74/Product: dermaseptine B3 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.Molecule type: protein
A.Molecule type: Drotein
A.Residues: 46.78 - 02Lb.
C.Superfamily: dermaseptin precursor; dermorphin precursor amino-terminal homology
C.Superfamily: dermaseptin precursor skin
C.Superfamily: dermorphin precursor amino-terminal homology contain: dermorphin precursor amino-terminal homology contain: elemental precursor amino-terminal homology contains: signal sequence #status predicted contain: propeptide #status predicted contain: propeptide #status predicted contain: propeptide #status predicted contain: adenoregulin #status experimental cMAT>
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C;Species: Phyllomedusa bicolor (two-colored leaf frog)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10456
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45.8%; Pred. No. 0.00041;
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22; Conservative
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Fig. 91 Product: dermorphin repeat (Partial) Fig. 91 Product: dermorphin #Status experimental 
Fig. 91 Product: dermorphin #Status experimental Fig. 94 Modified site: Dalanine (Ala) #Status experimental 
Fig. 94 Modified site: Dalanine (Ala) #Status experimental Fig. 94 Modified site: Dalanine (Ala) #Status experimental 
Fig. 94 Modified site: Dalanine (Ala) #Status experimental 
Fig. 94 Modified site: amidated carboxyl end (Ser) (amide in mature form from following gl Fig. 94 Modified site: amidated carboxyl end (Ser) (amide in mature form from following gl Fig. 94 Modified site: amidated carboxyl end (Ser) (amide in mature form from following gl Fig. 94 Modified site: amidated carboxyl end (Ser) (amide in mature form from following gl Fig. 94 Modified site: amidated carboxyl end (Ser) (amide in mature form from following gl Fig. 94 Modified site: amidated carboxyl end (Ser) (amide in mature form from following gl Fig. 94 Modified site: amidated carboxyl end (Ser) (amide in mature form from following gl Fig. 94 Modified site: amidated carboxyl end (Ser) (amide in mature form from following gl Fig. 94 Modified site: amidated carboxyl end (Ser) (amide in mature form from following gl Fig. 94 Modified site: amidated carboxyl end (Ser) (amide in mature form from following gl Fig. 94 Modified site: amidated carboxyl end (Ser) (amide in mature form from follow
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C;Comment: The precursor contains tandem repeats separated by paired basic residues as i
vity.
Science 238, 200-202, 1987
A;Title: D-alanine in the frog skin peptide dermorphin is derived from L-alanine in the A;Reference number: A94297; MUID:88017999; PMID:3659910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology C;Keywords: amidated carboxyl end; D-amino acid; neuropeptide; skin; tandem repeat F;1-47/Domain: dermorphin precursor amino-terminal homology <DER>
F;26-62/Domain: dermorphin repeat <RPTI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MFTLKKSLLLLFFLGTINLSLCEEERDADEERRDDLEERDVEVE-KRF 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.5%; Score 99.5; DB 2; Length 198; 45.8%; Pred. No. 0.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22; Conservative
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                                                                                                                                                                                                                                                                                           A; Residues: 1-198 <RIC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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F;96-130/Domain: dermorphin repeat <RPT3>
F;115-121/Product: dermorphin #status experimental <MAT2>
F;115-121/Product: dermorphin #status experimental <MAT3>
F;115-121/Product: dermorphin #status experimental <MAT3>
F;150-135/Product: dermorphin #status experimental <MAT3>
F;166-137/Domain: dermorphin #status experimental <F;49/Modified site: D-malanine (Ala) #status experimental
F;64/Modified site: amidated carboxyl end (Ser) (amide in mature form fron following glyce of the sundated carboxyl end (Ser) (amide in mature form fron following glyce)
F;115/Modified site: D-alanine (Ala) #status experimental
F;151/Modified site: D-alanine (Ala) #status experimental
F;156/Modified site: D-alanine (Ala) #status experimental
F;151/Modified site: D-alanine (Ala) #status experimental
F;151/Modified site: D-alanine (Ala) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Richter, K.; Egger, R.; Negri, L.; Corsi, R.; Severini, C.; Kreil, G. Proc. Natl. Acad. Sci. U.S.A. 87, 4836-4839, 1990
A;Title: cDNAs encoding [D-Ala(2)]deltorphin precursors from skin of Phyllomedusa bicolom A;Reference number: A35514; MUID:90280471; PMID:2352951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: A23723
A;Molecule type: mRNA
A;Residues: 1-645. KHDA.
A;Cross-treferences: UNIPROT:P13667; GB:J05016; NID:g181507; PIDN:AAA58460.1; PID:g181508
A;Cross-treferences: UNIPROT:P13667; GB:J05016; NID:g181507; J.
B;Huang, S.H.; Tomich, J.M.; Wu, H.; Jong, A.; Holcenberg, J.
J. Biol. Chem. 264, 14762-14768, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-227 <RIC>
A;Cross-references: UNIPROT:P21850; GB:M34560; NID:g213540; PIDN:AAA49451.1; PID:g213541
C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology
C;Keywords: skin
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C;Species: Phyllomedusa bicolor (two-colored leaf frog)
C;Date: 31-Oct.1990 #sequence_revision 31-Oct.1990 #text_change 09-Jul-2004
C;Accession: A35514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapв
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSFLKKSLLLIFLFLGLVSLSVCKEERRETEEENENEENHEEGSEMKRYMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.0%; Score 98; DB 1; Length 197; 44.0%; Pred. No. 0.0015; ive 11; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 31.4%; Score 96; DB 2; Length 227; 1 Similarity 46.9%; Pred. No. 0.0029; 23; Conservative 11; Mismatches 13; Indels
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Nature 390, 249-256, 1997
A,Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F., Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Fohl, T.M.; Portetelle, S.; Milester, M.; Rivolta, C.; Rochs, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Scanlon, A; Winters: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, T.; Winters: V. Winters: V. Winters, V.; Vata, K.; Yasanoto, W.; Vata, K.; Yoshida, K.; Attle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Reference number: A69580; MUID:98044033; PMID:9384377
A; Accession: G69850
A; Astatus: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:034725; GB:Z99110; GB:AL009126; NID:g2633472; PIDN:CAB13075.1
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 LKKSLLLLFFLGTINLSL--CEEERDADEERRDDLEERDVEVEK 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C, Superfamily: Bacillus subtilis hypothetical protein yjhA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          completed: March 30, 2005, 17:30:44
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Best Local Similarity 43.23
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-213 <KUN>
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                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: protein disulfide-isomerase; thioredoxin homology
C; Superfamily: protein disulfide-isomerase; thioredoxin homology
C; Keywords: duplication; endoplasmic reticulum; intramolecular oxidoreductase; isomerase
F; 12.2/Domain: signal sequence #status predicted <SIG>
F; 23.645/Product: endoplasmic reticulum protein ERp72 #status predicted <MAT>
F; 70-154/Domain: thioredoxin homology <TX1>
F; 785-265/Domain: thioredoxin homology <TX2>
F; 785-265/Domain: thioredoxin homology <TX2>
F; 787-645/Region: endoplasmic reticulum retention signal
F; 91-94, 206-209, 555-558/Disulfide bonds: redox-active #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Species: Helicobacter pylori
A; Variety: strain J99
C; Accession: F71896
C; Accession: F71896
R; Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; I ross, C.; Gibson, R., Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; A; Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A; Reference number: A71800; MUD:99120557; PMID:9923682
A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reaidues: 1-429 <ARN>
A;Cross-references: UNIPROT:Q9ZL62; GB:AB001503; GB:AE001439; NID:g4155275; PIDN:AAD063d
A;Experimental source: strain J99
C;Genetics:
A;Gene: jhp0718
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hypothetical protein yjhA - Bacillus subtilis
hypothetical protein yjhA - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: 669850
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
A;Title: Human deoxycytidine kinase. Sequence of cDNA clones and analysis of expression A;Reference number: A36508; MUID:89359272; PMID:2549034
                                                                                                                                    A;Residues: 1-609, TKRTQLNLRVETEIWS! <HU2>
A;Cross-references: GB:J05016
A;Note: this sequence has been corrected reference A23723
C;Comment: This sequence has no homology to deoxycytidine kinase (EC 2.7.1.74) and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein jhp0718 - Helicobacter pylori (strain J99)
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Matches 20; Conservative
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A;Gene: GDB:ERP70; ERP72
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Best Local Similarity
Matches 19; Conserv
                                                                                                       A; Molecule type: DNA
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Gaps

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14;

Score 69.5; DB Pred. No. 2.2; 8; Mismatches

DB 2; Length 213; Indels THIS PAGE BLANK (USPTO)

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March 30, 2005, 17:30:01; Search time 140 Seconds (without alignments) 144.265 Million cell updates/sec
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1 MFTLKKSLLLLFFLGTINLS......BVEKRFFPVIGRILNGILGK
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1: \cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: \cgn2_6/ptodata/2/pubpaa/PCT_MEW_PUB.pep:*
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6: \cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
7: \cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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18: \cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
19: \cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                          Run on:
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	Description	Sequence 16, Appl	Sequence 2, Appli	Sequence 8, Appli	Sequence 16475, A	Sequence 6289, Ap	Sequence 6290, Ap	Sequence 45818, A	Sequence 17, Appl	Sequence 245431,	Sequence 10903, A	Sequence 57178, A	Sequence 811, App	Sequence 32735, A
	σī	5 US-10-719-623-16	US-10-719-623-2	US-10-421-635-8	US-10-369-493-16475	US-10-335-977-6289	US-10-335-977-6290	US-10-282-122A-45818	US-10-719-623-17	US-10-424-599-245431	US-09-815-242-10903	US-10-282-122A-57178	US-10-408-765A-811	US-10-029-386-32735
		15	15	15	15	15	15	15	15	15	0	15	16	14
	Query Match Length DB	61	78	24	1039	429	430	1189	13	193	1192	1192	1684	59
do	Query Match	100.0	33.7	31.0	23.0	22.9	22.9	22.1	21.6	21.6	21.4	21.4	20.9	20.6
	Score	306	103	95	70.5	70	70	67.5	99	99	65.5	65.5	64	63
	Result No.	1	7	m	4	ŋ	9	7	ω	0	10	11	12	13

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531, 531, 9, A 3957 1131, 6521	V 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	e 37, A e 2237, e 160, e 160, e 160, e 160,	9999999	160, 160, 160, 160,
US-09-925-302-5 US-09-925-302- US-10-428-487- US-10-425-114- US-09-764-864-1 US-10-425-114-	4 4 4 4 4 4 A A	2-129 3-245 8-072 0-808 1-049 0-470	US-10-175-746-1 US-10-176-918-1 US-10-176-921-1 US-10-137-865-1 US-10-142-431-1 US-10-143-114-1	
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ALIGNMENTS

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RESULT 1
US-10-19-623-16
US-10-19-623
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US-10-369-493-16475
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US-10-335-977-6289
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Sequence 8, Application US/10421635;
Sequence 8, Application US/10421635;
Publication No. US20040064847A1
| GENERAL INFORMATION:
| TITLE OF INVENTION: Transgenic Plants Exhibiting Resistance to a Spectrum TITLE OF INVENTION: of Pathogens | Sea | CURRENT APPLICATION NUMBER: US/09/616,110 |
| PRIOR APPLICATION NUMBER: US/09/616,110 |
| PRIOR FILING DATE: 1099-11-12 |
| NUMBER OF SEQ ID NOS: 11 |
| SOFTWARE: Patentin Ver. 2.1 |
| SEQ ID NO 8
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31.0%; Score 95; DB 15; Length 24;
Best Local Similarity 75.0%; Pred. No. 0.00025;
Matches 18; Conservative 5; Mismatches
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Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Phyllomedusa bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Rana temporaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
US-10-369-493-16475
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Gladman, Baarry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/369,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 16475
LENGTH: 1039
TYPE: n.m.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.0%; Score 70.5; DB 15; Length 1039; 41.2%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6289, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEX: unsure
LOCATION: (1)..(1039)
OTHER INFORMATION: unsure at all Xaa locations
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COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
COMPATING SYSTEM: Windows NT 4.0
SOFFWARE: UNIX
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 10031
CORRESPONDENCE PADRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ 1D NO: 6289: SEQUENCE CHARACTERISTICS: LENGTH: 429 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Bacillus thuringlensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 41.2
Matches 21; Conservative
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JS-10-282-122A-45818
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                                                                                                                                                                                                                                                                                                                                                               RELATING TO HELICOBACTER PYLORI FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                Query Match 22.9%; Score 70; DB 15; Length 429; Best Local Similarity 41.3%; Pred. No. 6.6; Matches 19; Conservative 6; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 70; DB 15; Length 430;
Pred. No. 6.6;
                                                                                                                                                                                                                                         10 LLFFLGTINLSLCEEERDADEERRDDLEERDVEVEKRFFPVIGRIL 55
                                                         ; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...429
; SEQUENCE DESCRIPTION: SEQ ID NO: 6289:
US-10-335-977-6289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ). NAME/KEY: misc feature
; LOCATION: (B) LÖCATION 1...430
; SEQUENCE DESCRIPTION: SEQ ID NO: 6290:
US-10-335-977-6290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIW TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
                 ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 430 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 6290:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 22.9%;
Best Local Similarity 41.3%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: UNIX
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                    US-10-335-977-6290
                                                  FEATURE
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APPLICANT: Misra and Kay TITLE OF INVENTION: Trangenic Plants that are Resistant to a Broad Spectrum TITLE OF INVENTION: of Pathogens FILE REFERENCE: 673243 CURRENT APPLICATION NUMBER: US/10/719,623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Identification of Essential Genes in Microorganisms File REPRENCE. ELITRA, 0.94A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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Best Local Similarity 39.2%; Pred. No. 42;
Matches 20; Conservative 7; Mismatches
Sequence 45818, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/191, 078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PELICATION NUMBER: 60/206, 848
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR APPLICATION NUMBER: 60/230, 335
PRIOR PILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/245, 578
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-12-05
PRIOR PILING DATE: 2001-12-05
PRIOR PILING DATE: 2001-12-05
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-06
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Publication No. US20040073977A1
                                                                                             APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                    Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Bacillus anthracis
                                                                                                                                                                                                                                                       Zyskind, Judith
Wall, Daniel
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Gaps

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21; Indels

6; Mismatches

10 LLFFLGTINLSLCEEERDADEERRDDLEERDVEVEKRFFPVIGRIL 55

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APPLICANT: Yayking, Udulth,
APPLICANT: Yayking, Udulth,
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: You, H.
APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
APPLICANT: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/206,335
PRIOR PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-06
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                       CURRENT FILING DATE: 2017.078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/207, 727

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: PRESCE FOR WINDOWS VERSION 4.0

SECTION 10903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.4%; Score 65.5; Dilarity 34.5%; Pred. No. 74; Conservative 6; Mismatches
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Publication No. US20040029129A1
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US-09-815-242-10903
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Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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Best Local Similarity
Matches 20; Conserva
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Sequence 245431, Application No. US20040031072A1

GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwel
TITLE OF INVENTION: Blants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5323)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 245431
LENGTH: 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Obleson, Kari L.
APPLICANT: Consequence of the consequence 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.6%; Score 66; DB 15; Length 13;
100.0%; Pred. No. 0.34;
tive 0; Mismatches 0; Indels
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US-10-424-599-245431
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/125,072
PRIOR FILING DATE: 1999-03-17
PRIOR APPLICATION NUMBER: PCT/CA00/00288
PRIOR APPLICATION NUMBER: 90/936,885
PRIOR PILING DATE: 2000-03-16
PRIOR PLING DATE: 2001-09-17
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PATENTIN Ver. 2.0
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Batent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Rana temporaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Glycine max
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US-09-815-242-10903
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Fatent No. US20020044941A1

GENERAL INFORMATION:

APPLICANT: ROSen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

CURRENT APPLICATION NUMBER: US/09/925,302

CURRENT FILING DATE: 2001-08-10

PRIOR PLING DATE: 2001-08-10

PRIOR PLING DATE: 2000-03-08

PRIOR PLING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 896

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 531

LENGTH: 705
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: PRIOR NUMBER: 60/124,270
NUMBER OF SEQ ID NOS: 896
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 531
LENGTH: 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 705;
                                                                                                 DB 14; Length 59
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.7; CTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 7.5 US-10-029-386-32735
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                                                                                            Score 63; DB 1
Pred. No. 4.5;
8; Mismatches
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3; Mismatches
                                                                                                                                                                                        23 EEERDADEERRDDLEERDVEVEKRFFPVIG 52
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Pred. No. 91
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Publication No. US20030064072A9
GENERAL INFORMATION:
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Best Local Similarity 51.9%;
Matches 14; Conservative
                                                                                            Query Match
Best Local Similarity 40.0°
Matches 12; Conservative
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Matches 14; Conservative
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CORGANISM: Homo sapiens
US-09-925-302-531
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US-09-925-302-531
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US-10-029-386-32735
US-10-029-386-32735
Sequence 32735, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITTLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: US/10/029,386
CURRENT APPLICATION NUMBER: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 57178
LENGTH: 1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ghosh, Soumitra S.
APPLICANT: Chosh, Soumitra S.
APPLICANT: Eahy, Edin D.
APPLICANT: Zhang, Bing
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary W.
APPLICANT: Glenn, Gary W.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE REFERENCE: 660089.465
CURRENT APPLICATION WHERE: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 911
LENGTH: 1684
                                                                                                                                                                                                           Score 65.5; DB 15; Length 1192;
Pred. No. 74;
6; Mismatches 15; Indels 17;
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Pred. No. 1.7e+02;
4; Mismatches 7; Indels
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113 EEEEEDEERKOSDEERQKKKKR 136
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OTHER INFORMATION: MAP TO AC004493.1
                                                                                                               ; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-10-282-122A-57178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.9%;
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21.4%;
Best Local Similarity 34.5%;
Matches 20; Conservative
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Best Local Similarity 54.2
Matches 13; Conservative
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US-10-408-765A-811
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ORGANISM: Homo sapiens
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LENGTH: 59
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Search completed: March 30, 2005, 17:42:51 Job time : 141 secs

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576, Ap
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108.419 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Sequence 3
Sequence 5
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Sequence
Sequence
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                                                                                                                        March 30, 2005, 17:21:25 ; Search time 42 Seconds
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/AB_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-336-885A-15

US-09-319-730-17

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US-09-319-730-17

US-09-319-730-7

US-09-319-730-7

US-09-313-090-548

US-09-134-000C-5756

US-08-133-090-548

US-08-135-090-548

US-08-155-33-13

US-08-424-0178-13

US-09-248-756A-19128

US-09-248-756A-19128

US-09-248-766A-19128

US-09-134-001C-5527

US-09-134-001C-5527

US-09-243-608-2

US-09-243-608-2

US-09-243-608-2

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US-09-543-681A-5241
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Sequence 16, Application US/0993685A

Sequence 16, Application US/0993685A

Sequence 16, Application US/0993685A

Sequence 16, Application US/0993685A

TITLE OF INVENTION:
TITLE OF INVENT
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Sequence 876, App
Sequence 10896, A
Sequence 1130, Ap
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5754, Ap
9, Appli
10817, A
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22150, A
                                                                                                                                                              4, Appl
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; Sequence 19, Application US/09319730
; Ratent No. 6310176
; GENERAL INFORMATION:
APPLICANT: BARRA, Donatella
APPLICANT: SIMMACO, MAULIZIO
TITLE OF INVENTION: ANTIMICROBIALLY ACTIVE POLYPEPTIDES
FILE REFERENCE: 003300-574
; CURRENT APPLICATION NUMBER: US/09/319,730
CURRENT FILING DATE: 1999-08-24
PRIOR FILING DATE: 1999-18-12
; PRIOR FILING DATE: 1996-12-13
; WUMBER: OF SEQ ID NOS: 19
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 19
; LENGTH: 61
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                                                                                     US-09-248-796A-18781
US-09-248-796A-18990
US-08-056-200-94
US-08-638-092-1280
US-09-538-092-1280
US-09-328-352-5754
US-09-948-796A-25881
US-09-248-796A-25881
US-09-248-796A-25881
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US-09-585-645A-42
US-09-538-092-876
US-09-95-016-10896
US-09-538-092-1130
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100.0%; Pred. No. 7.8e-31;
ive 0; Mismatches 0;
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ORGANISM: Rana Temporaria
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Best Local Similarity
Matches 61; Conserv
61
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
LENGTH: 58
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                                                                                      TYPE: PRT
ORGANISM: Rana Temporaria
US-09-319-730-17
NUMBER OF SEQ ID NOS:
                                                                                                                                                                          Query Match
Best Local Similarity
Matches 45; Conserv
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US-09-936-885A-2
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                                                                                                                                                                                                                                                                                         1 MFTLKKSLLLLFFLGTINLSLCEEERDADEERRDDLEERDVEVEKFFFPVIGRILNGILG
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                                                                                                                                                                                                 100.0%; Score 306; DB 4; Length 61; 100.0%; Pred. No. 7.8e-31; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 15, Application US/09319730; Sequence 15, Application US/09319730; Patent No. 6310176; GENERAL INFORMATION; APPLICANT: BARRA, Donatella; APPLICANT: SIMMACO, Maurizio; FILE OF INVENTION: ANTIMICROBIALLY ACTIVE POLYPEPTIDES; FILE REPERENCE: 003300-574; CURRENT APPLICATION NUMBER: US/09/319,730; CURRENT PILING DATE: 1999-08-24; PRIOR APPLICATION NUMBER: PCT/SE97/02075; PRIOR APPLICATION NUMBER: SE 9604593-5; PRIOR PLLING DATE: 1997-12-12; PRIOR PLLING DATE: 1996-12-13
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| Patent No. 6310176
| Patent No. 6310176
| GENERAL INFORMATION:
| APPLICANT: SIMMACO, Maurizio
| TITLE OF INVENTION: ANTIMICROBIALLY ACTIVE POLYPEPTIDES:
| FILE REFERENCE: 003300-574
| CURRENT APPLICATION NUMBER: US/09/319,730
| CURRENT FILING DATE: 1999-08-24
| PRIOR APPLICATION NUMBER: PCT/SE97/02075
| PRIOR PILING DATE: 1997-12-12
| PRIOR PILING DATE: 1996-12-13
PRIOR FILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 61
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 61; Conservative
                                                                                                             TYPE: PRT
ORGANISM: Rana temporaria
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US-09-319-730-15
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US-09-319-730-17
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GENERAL INFORMATION:
APPLICANT: Misra and Kay
TITLE OF INVENTION: Trangenic Plants that are Resistant to a Broad Spectrum
TITLE OF INVENTION: ef Pathogens
FILE REFERENCE: 60993
CURRENT APPLICATION NUMBER: uS/09/936,885A
CURRENT APPLICATION NUMBER: 60/125,072
PRIOR APPLICATION NUMBER: PCT/CA00/00288
PRIOR FILING DATE: 1999-03-17
PRIOR APPLICATION NUMBER: PCT/CA00/00288
PRIOR FILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PARCHIN Ver. 2.0
SEQ ID NO : 20
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Sequence 920, Application US/09538092

Patent No. 6753314

GENERAL INFORMATION:
APPLICANT: Glot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same;
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT APPLICATION NUMBER: 60/127,352
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR APPLICATION NUMBER: 60/177,352
PRIOR APPLICATION NUMBER: 60/177,352
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 1387

SEQ ID NO 920

LENGTH: 645

TYPE: PRI
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Length 58;
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                                                     Indels
71.7%; Score 219.5; DB 3;
73.8%; Pred. No. 3.7e-20;
iive 7; Mismatches 6;
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33.7%; Score 103; DB 4;
Best Local Similarity 56.8%; Pred. No. 1.4e-05;
Matches 21; Conservative 8; Mismatches 6
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TYPE: PRT
ORGANISM: Homo sapiens
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NAME/KEY: UNSURE
LOCATION: 126
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       US-09-936-885A-17
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US-09-936-885A-17

Sequence 17, Application US/09936885A

Patent No. 6835868

GENERAL INFORMATION:

APPLICANT: Misca and Kay

TITLE OF INVENITON: Trangenic Plants that are Resistant to a Broad Spectrum

TITLE OF INVENITON: Of Pathogens

FILE REFERENCE: 60993

CURRENT APPLICATION NUMBER: US/09/936,885A

CURRENT APPLICATION NUMBER: 60/125,072

PRIOR PILING DATE: 1999-03-17

PRIOR PILING DATE: 1999-03-16

PRIOR FILING DATE: 2001-09-17

PRIOR FILING DATE: 2000-03-16

NUMBER OF SEQ ID NOS: 42

SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                              Query Match
23.0%; Score 70.5; DB 4; Length 645;
Best Local Similarity 28.2%; Pred. No. 1.5;
Matches 20; Conservative 10; Mismatches 16; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 7, Application US/09319730; Sequence 7, Application US/09319730; Patent No. 6310176; GENERAL INFORMATION; APPLICANT: BARRA, Donatella; APPLICANT: BARRA, Donatella; APPLICANT: SIMMACO, Maurizio; TITLE OF INVENTION: ANTIMICROBIALLY ACTIVE POLYPEPTIDES; FILE REFERENCE: 003300-574; CURRENT APPLICATION NUMBER: US/09/319,730; CURRENT FILING DATE: 1999-08-24; PRIOR APPLICATION NUMBER: PCT/SE97/02075; PRIOR APPLICATION NUMBER: SE 9604593-5; PRIOR FILING DATE: 1996-12-13; NUMBER OF SEQ ID NOS: 19; SEQ ID NOS: 19; SEQ ID NO 7; SEQ ID NO 7;
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                                    NAME/KEY: misc_feature
) LOCATION: (0)...(0)
) OTHER INFORMATION: Polypeptide Accession Number P13667
US-09-538-092-920
                                                                                                                                                                                                                                                          5 KKSLLLFFLGTINLSLCE-----
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ORGANISM: Rana temporaria
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| 65
ORGANISM: Homo sapiens
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US-09-319-730-7
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
FRIOR APPLICATION NUMBER: US 60/055,778
FRIOR FILING DATE: 1997-08-15
NUMBER: OF SEQ ID NOS: 6812
SOFTWARE: PACENTIN VETSION 3.1
SEQ ID NO 5756
LENGTH: 1208
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APPLICANT: Dunds Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PRICE REFERENCE: 59.US2.REG
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR PLING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 5448
LENGTH: 166
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Pred. No. 13;
6; Mismatches 15; Indels 17; Gaps
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  21.6%; Score 66; DB 4; Length 13; 100.0%; Pred. No. 0.071; ive 0; Mismatches 0; Indels
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LOCATION: 94
OTHER INFORMATION: Xaa=ABP or Glu or Gly
                                                                                                                                                                                                                                                                                                 Sequence 5756, Application US/09134000C Patent No. 6617156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5648, Application US/09513999C Patent No. 6783961
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LOCATION: 92
OTHER INFORMATION: Xaa=ABp or Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 21.4%;
Best Local Similarity 34.5%;
Matches 20; Conservative
Query Match
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                               47 FFPVIGRILNGIL 59
                                                                                                                                                 1 FFPVIGRILNGIL 13
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TITLE OF INVENTION: THEREOF
                                                                                                               CITY: Washing
STATE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
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US-08-319-152A-29

US-08-319-152A-29

Sequence 29, Application US/08339152A

Sequence 29, Application US/0831A

APPLICANT: Road N. Sequence 29, Application US/0831A

TITLE OF INVENTION: From The Amyloid -Protein Precursor (APP) Promoter UNMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:
                                                                                                                      Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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APPLICANT: Bupp, Keith
APPLICANT: Magendantz, Margaret
APPLICANT: Tanzi, Rudolph
APPLICANT: Solomon, Frank
TITLE OF INVENTION: AMYLOID PRECURSOR-LIKE PROTEIN AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 706;
                                                                        DB 4; Length 166;
                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 New York Ave., NW, Suite 600 STATE: DC STATE: DC CONTROLLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CONFUREN: APELICATION DATA:
APPLICATION NUMBER: US/08/339,152A
FILING DATE: 10-NOV-1994
FLING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTATION NUMBER: 36,688
REGISTATION NUMBER: 36,688
REGISTATION NUMBER: 36,688
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 202-371-2540
                                                                   Query Match
20.4%; Score 62.5; Di
Best Local Similarity 51.9%; Pred. No. 3.3;
Matches 14; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.4%; Score 62.5; 51.9%; Pred. No. 17
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Parent No. 5851787
GENERAL INFORMATION:
  ; OTHER INFORMATION: Xaa=His or Arg
US-09-513-999C-5648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 706 amino acida
TYPE: amino acid
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Best Local Similarity
Matches 14; Conserval
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US-08-007-999B-4
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NUMBER OF SEQUENCES: 19

CORMERS OF SEQUENCES: 19

ADDRESSES: Sterner, Keeler, Goldetein & Pox, P.L.L.C.
ADDRESSES: Sterner, Keeler, Goldetein & Pox, P.L.L.C.
CONTENT: 1100 New York Ave. NW

CONTENT: 100 New York No. 100 No.
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1;
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Patent No. 5677146

GENERAL INFORMATION:

APPLICANT: Foreter, Donald C

APPLICANT: Sprecher, Cindy

APPLICANT: No. 5677146ris, Kjeld

APPLICANT: No. 5677146ris, Kjeld

TITLE OF INVENTION: NOVEL HUMAN AMYLOID PROTEIN PRECURSOR

TITLE OF INVENTION: HOMOLOG AND KUNITZ-TYPE INHIBITOR

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: ZymoGenetics, Inc.

STREET: A4225 Roosevelt Way, N.E.

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98105
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PATENTIN Release #1.0, Version #1.25
GURRENT APPLICATION DATR:
APPLICATION NUMBER: US/08/424,022
                                                                                                                                             Query Match
20.4%; Score 62.5; I
Best Local Similarity 51.9%; Pred. No. 18;
Matches 14; Conservative 3; Mismatches
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216 EEEEDEEEEED-EEEDYDVYKSEFP 241
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CLASSIFICATION: 514
PRIOR APPLICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,692
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: PARKET, GATY B
REGISTRATION NUMBER: 31-684
REFERENCE/DOCKET NUMBER: 92-21C2
TELECHOME: 206-547-8080 ext 322
TELEFRAX: 206-548-2329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: March 30, 2005, 17:31:32
: 763 amino acids
amino acid
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Best Local Similarity 51.9°
Matches 14; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                         ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-155-331-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-424-022-13
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20.4%; Score 62.5; DB 2; Length 706;
Best Local Similarity 51.9%; Pred. No. 17;
Matches 14; Conservative 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Foster, Donald C
APPLICANT: Spreeher, cind C
APPLICANT: No Spreeher, cind C
APPLICANT: No Spreeher, cind C
TITLE OF INVENTION: NOVEL HUMAN AMYLOID PROTEIN PRECURSOR
TITLE OF INVENTION: HOMOLOG AND KUNITZ-TYPE INHIBITOR
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CUNTRY: SEGULIE

COUNTRY: USA

COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/155,331
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/985,692
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: PARKEY, GATY E
REGISTRATION NUMBER: 31-684
REFERENCE/DOCKET NUMBER: 32-11C1
TELEPHONE: 206-547-8080 ext 322
TELEFRAX: 206-547-8080
SEQUENCE CHARACTERISTICS:
               PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/007,999
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,642
FILING DATE: 20-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,022
FILING DATE: 17-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: JORGE A. GOLDSTEIN
REGISTRATION NUMBER: 29,021
RESERENCE/DOCKET NUMBER: 0609.3520003
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 EEEEDEEEEEED-EEEDYDVYKSEFP 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 EEERDADEERRODLEERDVEVEKRFFP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: ZymoGenetics, Inc. STREET: 4225 Roosevelt Way, N.B. CHIY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/08155331
Patent No. 5441931
                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 706 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-689-276A-4
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US-08-155-331-13
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OM protein - protein search, using sw model

March 30, 2005, 17:11:55; Search time 171 Seconds (without alignments) 137.967 Million cell updates/sec Run on:

US-10-719-623A-16

Title: Perfect score: Sequence:

306 1 MFTLKKSLLLLFFLGTINLS......BVEKRFFPVIGRILNGILGK

61

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

2105692 Total number of hits satisfying chosen parameters: 2105692 seqs, 386760381 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* 1: genesecnleser. Database :

geneseqp1980s:* geneseqp2000s:* geneseqp2001s:* geneseqp2001s:* geneseqp2001s:* geneseqp2003bs:* geneseqp2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	uo.	Rana temp	A tempori	Rana temp		A dermase	Pro-regio	Amino aci	Human int	Human PRO	Tumour-as	Human PRO	Novel hum	Novel hum	Bacterial	H. pylori	H. pylori	A thalian	Human tra	Novel hum	Protein e	Amino aci	Novel hum	Novel hum	Novel hum	Novel hum
	Description	Aaw51843	Aab18737	Aaw51841	Aaw51842	Aab18724	Aag62384	Adr88893	Aag66531	Ado19794	Abm80947	Adp56088	Aau30243	Aau30491	Ads27442	Aay10949	Aaw20585	Adm57239	Aay57950	Aau30488	Abu17894	Aab18738	Abg03927	Abg02975	Abg05363	Abg06330
	ID	AAW51843	AAB18737	AAW51841	AAW51842	AAB18724	AAG62384	ADR88893	AAG66531	ADO19794	ABM80947	ADP56088	AAU30243	AAU30491	ADS27442	AAY10949	AAW20585	ADM57239	AAY57950	AAU30488	ABU17894	AAB18738	ABG03927	ABG02975	ABG05363	ABG06330
	DB	7	ო	~	~	m	4	æ	4	œ	œ	8	4	4	ω	N	0	œ	m	4	Q	ო	4	4	4	4
	Length	61	61	61	58	78	24	62	645	645	645	645	646	918	1039	429	430	1512	605	91	1189	13	122	164	164	199
æ	Query	100.0	100.0	80.1	71.7	33.7	31.0	30.1	23.0	23.0	23.0	23.0	23.0	23.0	23.0	22.9	22.9	22.5	22.2	22.1	22.1	21.6	21.6		21.6	21.6
	Score	306	306	245	219.5	103	95	92	70.5	70.5	70.5	70.5	70.5	70.5	70.5	70	70	69	68	67.5	67.5	99	99	99		99
	Result No.	П	8	m	4	S	9	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Abb463101 Helicobac Abb46403 H. pylori Aau35310 Enterococ Abb407871 Enterococ Abb63283 Drosophill Aag30466 Arabidops Aag30466 Arabidops Aag30464 Arabidops Aag41602 Arabidops Aag41602 Arabidops Aag416005 Arabidops Aag416905 Arabidops Aag30464 Arabidops Aag31516 Arabidops Aag31516 Arabidops Aag33516 Arabidops Aag33161 Arabidops Abb64182 Drosophil	
ABU52101 AAB46342 AAB463310 AAU29254 ABU29254 ABU3283 AAG30466 AAG30466 AAG30466 AAG30466 AAG30316 AAG33517 AAG23516 AAG23516 AAG23516 ABB64182	ABOS9101 ABB68525 AAG44390 AAG44389
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283 429 429 11192 1208 1598 1599 1684 1684 211 2119 309	59 106 368 465
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2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	4 4 4 4 4 5 4 4 5 5 4 4 5 5 5 6 6 6 6 6

ALIGNMENTS

AAW51843 standard; protein; 61 AA. 26-OCT-1998 (first entry) AAW51843; AAW51843

Rana temporaria temporin G peptide.

Temporin G; anti-microbial property; anti-fungal property.

Rana temporaria.

1. .22 /note= "Signal peptide" Location/Qualifiers Key Peptide Protein

/note= "C-terminal amide present in the mature peptide" 47. .59 // Anture temporin G peptide; this peptide is claimed under claim 1 on page 20 in the specification. Modified-site

WO9825961-A1

18-JUN-1998.

97WO-SE002075. 12-DEC-1997;

96SE-00004593. (SBLV-) SBL VACCIN AB. 13-DEC-1996;

Barra D, Simmaco M;

WPI; 1998-362423/31. N-PSDB; AAV07449.

Peptides from the skin of the frog Rana temporaria - useful as anti-microbial or anti-fungal compositions.

Claim 1; Page 19, 20; 27pp; English.

The present sequence represents the Rana temporaria temporin G antimicrobial peptide encoded by the temporin G cDNA which was isolated from a R. temporaria skin cDNA library. The invention claims for other R. temporaria derived peptides which are claimed to be useful in medicaments for anti-microbial and anti-fungal use

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Rana temporaria temporin B peptide.
                                                                                     AAW51841 standard; protein; 61 AA.
                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                        (SBLV-) SBL VACCIN AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-362423/31.
N-PSDB; AAV07447.
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                                                                                                                                                                                                     Rana temporaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 61 AA;
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        61 K
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                                                                                                                                                                                                                                     Peptide
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Matches
                                                                           AAW5184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a temporin precursor polypeptide. The specification also describes dermaseptin polypeptides. Temporin and dermaseptin have antibacterial activity. Dermaseptin also inhibits fungal growth. Cationic peptides derived from temporins and dermaseptins are used to produce transgenic plants. The transgenic plants are useful for producing biologically active cationic peptides such as temporins and dermaseptins in large quantities. The peptide confers broad spectrum pathogen resistance including enhanced resistance to both fungal and bacterial pathogens in the transgenic plants. The transgenic plants may be used in conventional agricultural applications such as food crops, medical and other applications
                                                                           9
                                                                                          1 MPTLKKSLLLLFPLGTINLSLCEERDADEERRDDLEERDVEVEKRPPPVIGRILNGILG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transgenic plants resistant to broad spectrum of pathogens useful for producing biologically active cationic peptides, comprises nucleic acid molecule encoding temporin and/or dermaseptin peptides.
                                                                                                                                                                                                                                                                                           Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant; cationic peptide; pathogen resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MFTLKKSLLLLFFLGTINLSLCEEERDADEERRDDLEERDVEVEKRFFPVIGRILNGILG
                                                                           1 MFTLXKSLLLLFFLGTINLSLCEEERDADEERRDDLEERDVEVEKRFFPVIGRILNGILG
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                                Length 61;
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                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 306; DB 3;
1larity 100.0%; Pred. No. 3.2e-30;
Conservative 0; Mismatches 0;
                                                      ö
                              Score 306; DB 2;
Pred. No. 3.2e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
                             / Match 100.0%; Score 306; D
Local Similarity 100.0%; Pred. No. 3.2
Les 61; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 49-50; 58pp; English
                                                                                                                                                                                                                                                                        A temporin G precursor polypeptide.
                                                                                                                                                                                                      AAB18737 standard; protein; 61 AA.
                                                                                                                                                                                                                                                                                                                                                                                                   16-MAR-2000; 2000WO-CA000288
                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0125072P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-647077/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 61, Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kay WD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAA75750
                                                                                                                                                                                                                                                                                                                                Rana temporaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 61 AA;
         Sequence 61 AA;
                                                                                                                                                                                                                                                                                                                                                    WO200055337-A1
                                                                                                                       61 K 61
                                                                                                                                                                                                                                                                                                                                                                                                                         17-MAR-1999;
                                                                                                                                                                                                                                                  22-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                            21-SEP-2000
                                                                                                                                              61 K
                                                                                                                                                                                                                            AAB18737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misra S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                          /note= "C-terminal amide present in the mature peptide"
                                                                                                                                                                                                                           peptide is
specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MFTLKKSLLLLFFLGTINLSLCEEERDADEERRDDLEERDVEVEKRFFPVIGRILNGILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptides from the skin of the frog Rana temporaria - useful as anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 61;
Temporin B; anti-microbial property; anti-fungal property.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 80.1%; Score 245; DB 2; Length 61 Similarity 75.4%; Pred. No. 1.1e-22; 46; Conservative 9; Mismatches 6; Indels
                                                                                                                                                                                                                        /note= "Mature temporin B peptide; this claimed under claim 1 on page 20 in the
                                                                                                                                                                   note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           microbial or anti-fungal compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 18, 20; 27pp; English.
                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW51842 standard; protein; 58 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96SE-00004593.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-SE002075
                                                                                                                                                                                                47. .59
/note= "1
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AAW51842
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Misra S,
                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents the Rana temporaria temporin H antimicrobial peptide encoded by the temporin H cDNA which was isolated from a R. temporaria skin cDNA library. The invention claims for other R. temporaria derived peptides which are claimed to be useful in medicaments for anti-microbial and anti-fungal use
                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "C-terminal amide present in the mature peptide"
                                                                                                              47. .56
/note= "Mature temporin H peptide; this peptide is
claimed under claim 1 on page 20 in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant; cationic peptide; pathogen resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MFTLKKSLLLLFFLGTINLSLCEBERDADEBRRDDLEBRDVEVEKRFFPVIGRILNGILG
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                        Peptides from the skin of the frog Rana temporaria - useful as anti-
microbial or anti-fungal compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                  3.
                                                                                                                                                                                                                                                                                                                                                                                                71.7%; Score 219.5; DB 2; Length 58; 73.8%; Pred. No. 1.6e-19; ive 7; Mismatches 6; Indels
                                                        Temporin H; anti-microbial property; anti-fungal property.
                                                                                                      'note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                Claim 1; Page 18, 20; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dermaseptin precursor polypeptide
                                                                                       Location/Qualifiers
                                       Rana temporaria temporin H peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB18724 standard; protein; 78 AA.
                                                                                                                                                                                                97WO-SE002075
                                                                                                                                                                                                                96SE-00004593
                       26-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                  45; Conservative
                                                                                                                                                                                                                                (SBLV-) SBL VACCIN AB.
                                                                                                                                                                                                                                                Barra D, Simmaco M;
                                                                                                                                                                                                                                                                WPI; 1998-362423/31.
N-PSDB; AAV07448.
                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                        Rana temporaria
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 58 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K 58
                                                                                                                                        Modified-site
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                                                                                                                                                                                               12-DEC-1997;
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                                                                                                                                                                                                                13-DEC-1996;
                                                                                                                                                               WO9825961-A1
                                                                                                                                                                               18-JUN-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB18724;
      AAW51842
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                Peptide
                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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The present sequence represents a dermaseptin precursor polypeptide. The precursor is processed to produce two mature forms, dermaseptin b (AAB18725) and dermaseptin B (AAB18726). Dermaseptin has antibacterial activity, and inhibits fungal growth. Cationic peptides derived from transgenic plants fungal growth. Cationic peptides derived from transgenic plants are useful for producing biologically active cationic peptides such as temporins and dermaseptins in large quantities. The peptide confers broad spectrum pathogen resistance including enhanced resistance to both fungal and bacterial pathogens in the transgenic plants. The transgenic plants may be used in conventional agricultural applications such as food crops, medical and other applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transgenic plant; cationic peptide; cecropin-mellitin; CEMA; resistance; antibacterial; antifungal; antimicrobial; food crop; blight; soft rot; frog; temporin G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transgenic plants resistant to broad spectrum of pathogens useful for producing biologically active cationic peptides, comprises nucleic acid molecule encoding temporin and/or dermaseptin peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDILKKSLFLVLFLGLVSLSICEEEKRENEDEEKQDD 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MFTLKKSLLLLFFLGTINLSLCEER--DADEERRDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.7%; Score 103; DB 3; 56.8%; Pred. No. 6e-05; ive 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
                                                                                                                                                                                                                                                                                                                     (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 47; 58pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG62384 standard; peptide; 24 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pro-region of temporin G peptide.
                                                                                                                                                                                              16-MAR-2000; 2000WO-CA000288.
                                                                                                                                                                                                                                                               99US-0125072P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-JUL-2000; 2000WO-CA000826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0165249P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 56.8
1es 21; Conservative
Phyllomedusa bicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-647077/62.
                                                                                                                                                                                                                                                                                                                                                                                          Kay WD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAA75749.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rana temporaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 78 AA;
                                                             WO200055337-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200136647-A1
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                                                                                                                                                                                                                                                               17-MAR-1999;
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                                                                                                                              21-SEP-2000
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cationic peptide of the cecropin-mellitin (CEMA) family or related peptide. CEMA is an antimicrobial peptide with confers resistance to fungal and bacterial pathogens. Included in the invention are CEMArelated fusion peptide in which an N-terminal extension peptide is fused to the CEMA peptide. A pro-region peptide may be used as a fusion peptide, which meutralises the cationic nature of the CEMA or CEMArelated peptide and provides enhanced stability in cellular environments, or decreases the toxicity of the CEMA or CEMA-related peptide to the host organism. Transgenic plants of the invention may be used in conventional agricultural applications, such as food crops. The plants may display resistance to late blight due to Phytophthora infestans and or to soft rot due to Erwinia carctovara. The present sequence represents a temporin G pro region peptide, which can be used to modify the CEMA peptides used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tryptophyllin-1; PdT-1; vasodilatory; frog; defensive skin secretion; vasodilation; ischaemic heart disease; ischaemic disease; vasodilation; ischaemic heart disease; ischaemic disease; anti-cancer; anglogenesis; healing; transplant; graft; spinal cord injury; cardiovascular disease; arterial smooth muscle; spinal cord injury; cardiovascular disease; arterial smooth muscle; encreal nervous system disorder; infection; inflammation; cancer; tumour; haematopoietic malignancy; glaucoma; pulmonary hypertension; stroke; antherosclerosis; asthma; ophthalmologic disease; renal failure; menstrual disorder; obstetric condition; wound; gastroenteric disease; anaphylactic shock; endotoxic shock.
                                                                         Transgenic plants useful as food crops are resistant to late blight due to Phytophthora infestans and/or to soft rot due to Erwinia carotovara.
                                                                                                                                                                          present invention relates to a transgenic plant, which expressed a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.0%; Score 95; DB 4; Length 24; 75.0%; Pred. No. 0.00016; Live 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of tryptophyllin-1 designated PdT-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 EEERDADEERRODLEERDVEVEKR 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                   Disclosure; Page 51; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADR88893 standard; protein; 62 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2004; 2004WO-IB000806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-FEB-2003; 2003GB-00002621
  Osusky M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 75.0°
Matches 18, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pachymedusa dacnicolor.
                                      WPI; 2001-336007/35
  Kay WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2004074312-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24 AA;
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  Misra S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
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The present sequence represents a full length tryptophyllin-1, derived from Pachymedusa dacnicolor and designated PdT-1. The specification describes tryptophyllin-1 peptides are isolated from frog defensive skin secretions. Tryptophyllin-1 peptides are isolated from frog cefensive skin secretions. Tryptophyllin-1 peptides of the invention are useful for preparing a medicament for treating disorders where casedilation is beneficial, such as ischaemic heart disease, ischaemic disease of other organs or organ systems, vascular stenoses, occlusion to peripheral vessels, or hypertension, and for increasing the transport of biologically active compounds across the blood-brain barrier, where the biologically active compounds are nati-cencer drug. They are useful for promoting angiogenesis, for treating conditions of vascular useful for computing angiogenesis, for treating conditions of vascular constitutions and for treating sphnal cord injuries. They are also useful for treating cardiovascular disease, for increasing vasodilation, for treating sphnal cord injuries. They are also useful for combination with other therapeutic agents, peptides of the invention are useful for treating disorders in the brain including central nervous concer, tumour, Hodgkin's disease, non-Hodgkin's lymphomas, inflammation and magnetion are also useful in treating glaucoma, pulmonas, multiple mylence, atherosclerosis, asthma, ophthalmologic disease, renal disease, consistent conditions, wound, gastroenteric disease, conspination or endotoxic shock, etc...
                                                                                                                                                                                                                                                Isolated tryptophyllin peptide obtained from biologically active analog of Pachymedusa dacnicolor tryptophyllin-1, having vasodilatory activity, useful for treating conditions of vascular insufficiency e.g., ischemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; interferon-alpha induced gene; type I interferon treatment;
chronic viral hepatitis; relapsing remitting multiple sclerosis;
neoplastic disease; ERP-70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human interferon-alpha induced polypeptide, ERP-70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 18; 55pp; English.
                                                                                                                                                      O'rourke M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG66531 standard; protein; 645 AA
06-JUN-2003; 2003GB-00012990.
                                                                                                                                                      Shaw C, Hirst D, Chen T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                            WPI; 2004-642491/62.
N-PSDB; ADR88892.
                                     UNIV ULSTER SHAW C.
                                                                                                                   O'ROURKE M
                                                                           HIRST D.
CHEN T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 62 AA;
                                                                                                                                                                                                                                                                                                            heart disease.
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                                                         (SHAW/)
(HIRS/)
(CHEN/)
                                                                                                                 (OROU/)
                                       (UXUL-)
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Matches
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Gape

Homo sapiens

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Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
                systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis; autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis; diabetes mellitus; renal disease; demyelinating disease; central nervous system; peripheral nervous system; demyelinating polyneuropathy; dillain-Barre syndrome; chronic inflammatory demyelinating polyneuropathy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for treating and diagnosing immune related disorders in mammals. The immune related disorders include systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, systemic sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   central or peripheral nervous system, demyelinating polyneuropathy, Guillain-Barre syndrome and chronic inflammatory demyelinating polyneuropathy. This sequence represents a human PRO polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumour-associated antigenic target; TAT; human; overexpression; cancer; tumour; diagnosis; cell proliferative disorder; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumour-associated antigenic target (TAT) polypeptide PRO2733, SEQ:2443.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schoenfeld J, Williams PM;
osteoarthritis; juvenile chronic arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 8; Length 645;
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28.2%; Pred. No. 6.7;
ive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; SEQ ID NO 718; 1731pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Chiu H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABM80947 standard; protein; 645 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Clark H,
                                                                                                                                                                                                                                                                                                         06-NOV-2003; 2003WO-US035268.
                                                                                                                                                                                                                                                                                                                                                   08-NOV-2002; 2002US-0425235P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 28.2 les 20; Conservative
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rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                 GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 spondyloarthropathy.
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Wu TD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 645 AA;
                                                                                                                                                                                                                    WO2004043361-A2
                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                27-MAY-2004
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Wood WI,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method for predicting responsiveness of a patient to treatment with a type I interferon. The method comprises determining the level of one or more proteins with a 646, 164, 126, 598, 98, 177, 761, 361, 941, 657, 817, 429, 473, 399, 285 or 303 amino acid sequence fully defined in the specification after treatment with a type I interferon. The method allows a physician to determine whether a patient suffering from chronic viral hepatitis, neoplastic disease or relapsing remitting multiple sclerosis will respond favourably to Type I interferon treatment via oxomucosal administration. The present sequence is one of the polypeptides listed above that may be used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Predicting responsiveness of a patient to treatment with a type I interferon comprising determining the level of induced proteins after treatment with a type I interferon,.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 KKSLLLLFFLGTINLSLCE-------EERDADEERRDDLEERDVEVEKRFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.0%; Score 70.5; DB 4; Length 645; 28.2%; Pred. No. 6.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16; Indels
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11-FEB-2000, 2000GB-00003208.
11-FEB-2000, 2000GB-00003210.
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2000GB-00003222.
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11-FEB-2000; 2000GB-00003220.
                                                                              09-FEB-2001; 2001WO-GB000578
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11-FEB-2000; 2000GB-00003206
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11-FEB-2000; 2000GB-0003216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-483570/52
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Best Local Similarity
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셤 ò 셤 antiasthmatic; antidiabetic; antinflammatory; antipsortatic; antirhematic; antidiabetic; antinflammatory; antipsortatic; antirhyroid; CNS; dermatological; gastrointestinal; haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular; nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic; virucide; gene therapy.

response stimulation; antiallergic; antianaemic; antiarthritic;

PRO; immune related disease; inflammatory immune response;

Human PRO protein sequence SEQ ID NO:2064.

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coverexpressed in cancer tissues compared antigence dariger. Italy, overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosts and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide acquences at least 80¢ identical to the TAT nucleic acids and polypeptide acquences at least 80¢ identical to the TAT nucleic acids and polypeptide and polypeptides and polypeptides and polypeptides and polypeptides and polypeptides and polypeptides and polypeptides; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancer, liver cancer, bancer, colorectal cancer, lung cancer, cervical cancer, liver cancer, bancer, colorectal cancer, cervical cancer, inver cancer, bancer, cancer, seed as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence chromosome identification and in gene therapy. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human tumour-associated antigenic target (TAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumor-associated antigenic target polypeptides and nucleic acids,
colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical acacer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping; gene therapy; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful in preparing a medicament for treating or detecting a
proliferative disorder, e.g. breast, lung, colorectal, ovarian or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 8; Length 645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12; SEQ ID NO 2443; 7273pp; English.
                                                                                                                                                                                                                                                                                  29-SEP-2003; 2003WO-US028547
                                                                                                                                                                                                                                                                                                                            02-OCT-2002; 2002US-0414971P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prostate cancer or tumor.
                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2004-347921/32.
                                                                                                                                                                                                                                                                                                                                                                                                                      Zhang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB, ACN38739
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                                                                                                                                                                                         WO2004030615-A2
                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                      15-APR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                      Wu TD,
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New PRO polynucleotides and polypeptides, useful in useful in diagnosing and treating an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in

Claim 1; SEQ ID NO 2064; 3009pp; English.

stimulating an immune response.

Gurney AL, Schoenfeld J, Williams PM;

Aggarwal S, Clark H, Wood WI, Wu TD; (GETH) GENENTECH INC

Wood WI,

WPI; 2004-376182/35. N-PSDB; ADP56087.

28-OCT-2003; 2003WO-US034381. 29-OCT-2002; 2002US-0422472P.

WO2004039956-A2. Homo sapiens.

13-MAY-2004.

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                                                                                    4 RKAFLLLLLIGLVQLLAVAGAEGPDEDSSNRENAIEDEEEEEEEDDDEEEDDLEVKEE-- 61
                                                                 5 KKSLLLLFFLGTINLSLCE-------EERDADEERRDDLEERDVEVEKRFF
                                          Gaps
                                        25;
                                        16; Indels
           23.0%; Score 70.5; DE 28.2%; Pred. No. 6.7; iive 10; Mismatches
Query Match
Best Local Similarity 28.2
Local 20; Conservative
                                                                                                                           23
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ADP56088 standard; protein; 645 AA.

RESULT 11 ADP56088

18-NOV-2004 (first entry)

ADP56088;

The present invention describes an isolated PRO nucleic acid (I). Also described: (1) a vector comprising (I); (2) a host cell comprising the vector of (1); (3) a process for producing a PRO polypeptides; (4) an cisolated PRO polypeptide; (5) a chimeric molecule comprising the cisolated PRO polypeptide; (5) a chimeric molecule comprising the composition of matter comprising a polypeptide of (4); an agonist or antagonist of the polypeptide or an antibody that binds to the composition of matter comprising a container, a label on the container and a composition of matter of (7); (9) a method of treating an immune related disease in a comprising a container, a label on the container and a composition of mammal; (10) a method for determining the presence of a PRO polypeptide or in a sample suspected of having the polypeptide; (11) a method of indentifying a compound that inhibits or comprising an immune related disease or an inflammatory immune response in a mammal; (12) a method of identifying a compound that inhibits or minics the activity of or expression of a gene encoding a PRO polypeptide; antidatheutic, antidiabetic, antidialement, antiahretic, antidiabetic, respiratory, vasorropic and virucide activities, and can be used in gene therapy. The nucleic acid (1) and the encoded polypeptides, compositions, kits and methods are useful in diagnosing and treating an immune related disease and inn custing the present sequence represents a human constitution. 4 RKAFLILLIGLVQLLAVAGAEGPDEDSSNRENAIEDEEEEEEEDDDEEEDDLEVKEE-- 61 5 KKSLLLLFFLGTINLSLCE------EERDADEERRDDLEERDVEVEKRFF 25; Gaps DB 8; Length 645; 16; Indels 23.0%; Score 70.5; DE 28.2%; Pred. No. 6.7; ive 10; Mismatches Local Similarity 28,2 les 20; Conservative Sequence 645 AA; Query Match Best Loca Matches ò 셤

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stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.

18-APR-2000; 2000US-00552929. 26-JAN-2001; 2001US-00770160.

16-APR-2001; 2001WO-US008656

Homo sapiens. WO200179449-A2.

25-OCT-2001.

gene therapy; nutritional supplement;

Novel human secreted protein #982.

18-DEC-2001

AAU30491;

Human; vaccination;

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AAU30491 standard; protein; 918

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ANUS910-ANU39304 represent the amino acid sequences of novel human secreted proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                                                  Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to novel human secreted polypeptides.
                                                                                 AAU30243 standard; protein; 646 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; Page 266; 765pp; English.
                                                                                                                                                          Novel human secreted protein #734.
                                                                                                                                                                                                                                                                                                         16-APR-2001; 2001WO-US008656
                                                                                                                                                                                                                                                                                                                                18-APR-2000; 2000US-00552929.
26-JAN-2001; 2001US-00770160.
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                                                                                                                                   (first entry)
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168 20; Conservative
49 PVIGRILNGIL 59
                     -----NGAT
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                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 646 AA;
                                                                                                                                                                                                                                                        WO200179449-A2.
                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                 18-DEC-2001
                                                                                                                                                                                                                                                                                25-OCT-2001.
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                                                                                                         AAU30243;
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                                                                                                                                                                                Human;
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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying at the rapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acides encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used a sumiritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or atimulation; as anti-inflammatory agents; and in treatment of leukaemias. AMU29510-AMU33304 represent the amino acid sequences of novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----EERDADEERRDDLEERDVEVEKRFF 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                   Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
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                                                                                                                                                                                                                                                                                                    Claim 20; Page 300; 765pp; English.
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                                                              Liu C, Drmanac RT;
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                                                                                                                                WPI; 2001-611725/70.
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(HYSE-) HYSEQ INC.
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                                                                     Tang
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RESULT 14 ADS27442

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Bacteria.
 ADS27442;
                        (SLAT/)
(CHEN/)
(GOLD/)
                      CAOY/)
                           Cao Y,
                       (HINK/)
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a comprising the recombinant DNA construct and a method of producing a transformed plant as maize or soybean. The method of producing a plant is a crop plant comprising the recombinant DNA construct and growing the transformed plant with the recombinant DNA construct and growing the transformed plant where the polymuclectide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for improving plant properties. CC The recombinant DNA construct is useful for improving plant properties. CC increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved plant growth and development under at least one stress production, improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved plant growth and development under a form the sequence repersents a bacterial polypeptide used in the grow part of the printed specification but was obtained in electronic form part of the printed specification but was obtained in electronic compared from USPTO at sequence. New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties. cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide. Recombinant DNA construct; transformed plant; improved plant property; Goldman BS; Claim 1, SEQ ID NO 16475; 122pp; English. Chen X, ADS27442 standard; protein; 1039 AA Hinkle GJ, Slater SC, Bacterial polypeptide #16475 20-FEB-2003; 2003US-00369493 21-FEB-2002; 2002US-0360039P (first entry) CAO Y. HINKLE G J. SLATER S C. CHEN X. GOLDMAN B S. WPI; 2004-061375/06. Sequence 1039 AA; JS2003233675-A1. 02-DEC-2004 18-DEC-2003.

Search completed: March 30, 2005, 17:26:46 Job time : 173 sec8 ઠ 셤 Gaps 7; Indels 17; 23.0%; Score 70.5; DB 8; Length 1039; 41.2%; Pred. No. 11; ive 6; Mismatches 7; Indels 17 Query Match 23.0 Best Local Similarity 41.2 Matches 21; Conservative

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Helicobacter pylori nucleic acids and proteins - used to develop products for the detection, prevention and treatment of H. pylori infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant or substantially pure preparations of H. pylori polypeptides are disclosed, together with the nucleic acids encoding them. In all, 73 ORFs are shown. The proteins are variously cell envelope proteins, secreted proteins or other cellular proteins. Vaccines containing the nucleic acids or proteins are claimed, as are probes containing at least 8 nucleotides from the nucleic acid sequences. The vaccines are useful for treating or reducing the risk of H. pylori infections, and the probes can be used disgnostically for detecting the presence of Helicobacter in a sample. The products are also of use in screening for compounds having the ability to interfere with the H. pylori life cycle or to inhibit H.
                                                                                                                                                                                                            Vaccine, probe, diagnostic, ORF, cell envelope protein, secreted protein,
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22.9%; Score 70; DB 2; Length 429; 41.3%; Pred. No. 4.9;
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                                                                                       AAY10949 standard; protein; 429 AA
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/cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:
/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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SUMMARIES	QI	US-10-719-623-15	US-10-719-623-1	US-10-027-632-185531	US-10-027-632-185531	US-09-864-408A-4267	US-10-357-930-30217	US-10-221-714A-520	US-10-027-632-3788	US-10-027-632-3788	US-10-311-455-1659	US-10-411-910A-116
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	Query Match	100.0	13.7	12.9	12.9	12.3	12.2	12.2	12.0	12.0	12.0	11.8
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	38.6	38.6	38.6	38.6	38.6	38.6	38.6	38.6	38.6	38.6	38.4	38	38	38	38	ċ	•	37	37	37	37	36.8	36.8	36.8	36.8	36.8	36.8	36.8	36.8	36.8	36.6	36.4	36.4
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ALIGNMENTS

| JAPPICANT: Misra and Kay | JAPPICANT: Misra and Kay | JAPPICANT: Misra and Kay | TITLE OF INVENTION: Trangenic Plants that are Resistant to a Broad Spectrum | TITLE OF INVENTION: of Pathogens | TITLE OF INVENTION: of Pathogens | FILE REFERENCE: 673243 | CURRENT APPLICATION NUMBER: US/10/719,623 | CURRENT PILING DATE: 2003:11-20 | FRIOR APPLICATION NUMBER: 60/125,072 | FRIOR PILING DATE: 1999-03-16 | FRIOR PILING DATE: 2000-03-16 | FRIOR PILING DATE: 2000-03-16 | FRIOR PILING DATE: 2001-09-17 | FRIOR PILING DATE: 2001-09-17 | FRIOR FILING DATE: 2001-09-17 | SOFTWARE: Patentin Ver. 2.0 | SEQ ID NO 15 | LENGTH: 329 | LENGTH: 329 | LENGTH: 329 ö 9 Gaps ö Length 329; Indels Query Match 100.0%; Score 329; DB 17; Best Local Similarity 100.0%; Pred. No. 3.9e-78; Matches 329; Conservative 0; Mismatches 0; Sequence 15, Application US/10719623
; Publication No. US20040073977A1
; GENERAL INFORMATION: TYPE: DNA ORGANISM: Rana temporaria) NAME/KEY: CDS ; LOCATION: (53)..(238) ,us-10-719-623-15 ઠે

1 CCCCTCCAGCTGTCTACATTCTCATAACCAACTGAACCACCCGAGCCCAAAGATGTTCAC

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CURRENT APPLICATION NUMBER: US/10/027,632
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                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Human
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; Sequence 1. Application US/2004007397A1
; Sequence 1. Application No. US2004007397A1
; GENERAL INFORMATION:
    APPLICANT: Misra and Kay
    TITLE OF INVENTION: Trangenic Plants that are Resistant to a Broad Spectrum
    TITLE OF INVENTION: Trangenic Plants that are Resistant to a Broad Spectrum
    TITLE OF INVENTION: Trangenic Plants that are Resistant to a Broad Spectrum
    TITLE OF INVENTION: Trangenic Plants that are Resistant to a Broad Spectrum
    TITLE OF INVENTION: Trangenic Plants to Spoil 1.20
    PRIOR FILING DATE: 2003-11-20
    PRIOR PILING DATE: 2000-03-16
    PRIOR PLING DATE: 2000-03-16
    PRIOR PLING DATE: 2001-09-17
    NUMBER OF SEQ ID NOS: 41
    SOFTWARE: Patentin Ver. 2.0
    SEG ID NOS: 41

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        1 CCCCTCCAGCTGTCTACATTCTCATAACCAACTGAACCACCCGAGCCCCAAAGATGTTCAC
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US-10-027-632-18531
US-10-027-632
Sequence 185531, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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Pred. No. 0.076;
0; Mismatches 35; Indels
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Best Local Similarity 65.3
Matches 66; Conservative
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; LOCATION: (58)..(294)
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Sequence 185531, Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION:

APPLICANT: Wang, David G

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: 108827.129

CURRENT PILING DATE: 2002-04.30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR PILING DATE: 2000-00-229

PRIOR PILING DATE: 2000-00-229

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-10-29

PRIOR PILING DATE: 1999-10-3

PRIOR PILING DATE: 1999-10
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12.9%; Score 42.4; DB 13; Length 665;
Best Local Similarity 53.7%; Pred. No. 0.46;
Matches 88; Conservative 0; Mismatches 76; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286 TGGAATGTCATTTAGCTAAATGCACATCAAATGTCTTATAAAA 329
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CURRENT AFPLICATION NUMBER: US COLORENT FILING DATE: 2002-04-30 PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12 PRIOR FILING DATE: 2000-04-20 PRIOR PILING DATE: 2000-04-20 PRIOR PILING DATE: 2000-03-29 PRIOR PILING DATE: 2000-03-29 PRIOR PLING DATE: 2000-03-24 PRIOR PILING DATE: 1999-04-20 PRIOR FILING DATE: 1999-04-28 PRIOR FILING DATE: 1999-04-28 PRIOR FILING DATE: 1999-08-09 PRIOR FILING DATE: 1999-08-09 NUMBER: US 60/16,358 PRIOR FILING DATE: 1999-08-09 NUMBER: OF SEQ ID NOS: 325720 SOFTWARE: PASSIE PRIOR PRI
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OTHER INFORMATION: n = A,T,C or G
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APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE REFERENCE: MRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR PELING DATE: 2000-03-16
PRIOR PLILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-12
PRIOR PRILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-11-13
NUMBER OF SEQ ID NOS: 62222
SOUTHARE: FRSESEQ FOR WINDOWS VERSION 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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; LOCATION: 4776, 4777, 4778, 4779, 4780, 4781, 4782, 4783, 4784,

; LOCATION: 4786, 4787, 4788, 4789, 4790, 4791, 4792, 4793, 4794,

; LOCATION: 4796, 4797, 4798, 4799, 4800, 4801, 4802, 4803, 4804

US-10-357-930-30217
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Publication No. US20040048254A1

GENERAL INFORMATION:

APPLICANT: OLEX, Alexander

APPLICANT: PIEBENBROCK, Christian

APPLICANT: BERLIN, Kurt

ITLE OF INVENTION: Lumor suppressor genes and oncogenes

FILE REFERENCE: 5013.1005

CURRENT FILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: US/10/221,714A

CURRENT FILING DATE: 2001-03-15

PRIOR PILING DATE: 2001-03-15

PRIOR PELING DATE: 2000-03-15

PRIOR PELING DATE: 2000-03-15

PRIOR PILING DATE: 2000-03-15

PRIOR PILING DATE: 2000-03-15

PRIOR PILING DATE: 2000-03-15

PRIOR PILING DATE: 2000-03-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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LENGTH: 4804
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US-09-664-408A-4267/c

1 Sequence 4267, Application US/09864408A

2 Sequence 4267, Application US/09864408A

3 GENERAL INFORMATION:

4 APPLICANT: Leach, Martin D.

5 APPLICANT: Shinkets, Richard A.

7 TILE OF INVENTION: No. US20040009474Alel Human Polynucleotides and Polypeptides Encc

7 FILE REFERENCE: 21402-012

7 CURRENT APPLICATION NUMBER: US/09/864,408A

7 CURRENT FILING DATE: 2001-05-24

7 PRIOR FILING DATE: 2000-05-24

7 NUMBER OF SEQ ID NOS: 9068

7 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                            166 AAGGGATGTTGAAGTGGAAAAGCGATTTTTTCCAGTGATTGGAAGGATACTCAATGGTAT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 TTTATGTAACATCAAACTATACTTATTTGAGGAAAATGAAATAATATTATAATT 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                   7 AAGATAATTTTAAAAATTGTTCTTTCCTAGTTCTTCCCATATCCATAACTAAAT 66
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                                                                                                                                                                                                                                                          Score 42.4; DB 17; Length 665;
Pred. No. 0.46;
0; Mismatches 76; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              286 TGGAATGTCATTTAGCTAAATGCACATCAAATGTCTTATAAAA 329
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                                                                                                         | NAME/KEY: misc_feature
| LOCATION: (1)...(665)
| OTHER INFORMATION: n = A,T,C or G
| US-10-027-632-185531
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 53.7%;
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 94; Conserv
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                        TYPE: DNA
ORGANISM: Human
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US-10-357-930-30217
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LENGTH: 665
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US-10-027-632-3788/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9356 ACTCCAATAACCATTTTCTACAATATCGTATTAATACTTAACAAATTTCAAATTTTAAA 9297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 AGIGGAAAAGCGAITITITCCAGIGATIGGAAGGAIACICAAIGGIAITITGGGAAAAIA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCAAAAAAAGTTAAAAACTTTGGAAATGGAATTGGAAATCATCTAATGTGGAATGTCATT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 10827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR PELICATION NUMBER: US 60/128,006
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-07-20
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-28
PRIOR PILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-38
PRIOR FILING DATE: 1999-10-38
PRIOR PILING DATE: 1999-10-38
PRIOR FILING DATE: 1999-10-38
PRIOR FILING DATE: 1999-10-38
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-38
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                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-221-714A-520
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
12.2%; Score 40; DB 17; Length 56153;
Best Local Similarity 53.9%; Pred. No. 16;
Matches 82; Conservative 0; Mismatches 70; Indels 0
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Pred. No. 3.3;
0; Mismatches 66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAGCTAAATGCACATCAAATGTCTTATAAAAA 329
PRIOR APPLICATION NUMBER: DE LOUSES.
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 540
SEQ ID NO 520
LENGTH: 56153
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                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 54.5
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-027-632-3788/c
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US-10-027-632-3788
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Sequence 1659, Application US/10311455
Sequence 1659, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DIEFENBROCK, Christian
TITLE OF INVENTION: cytosine methylation
FILE REFERENCE: 5013.1014
FILE REFERENCE: 5013.1014
CURRENT APPLICATION UNMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
FRIOR APPLICATION NUMBER: PCT/EP01/07537
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199 AGTGATTGGAAGATACTCAATGGTATTTGGGAAAATAACCAAAAAAAGTTAAAACTTT 258
                                                                 287 Aaricaaaaacaragacticcaggarrictragggaaggaaacaaacaaaagarriraggactrr 228
                                                                                                                                                                                                                                                                                                                                                                                                                   US-1U-UZ/-S148/C

SGENGERC 3788, Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICATION:

TITLE OF INVENTION: Tedentification and Mapping of Single Nucleotide

TITLE OF INVENTION: Tedentification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 10882.129

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2002-04-20

PRIOR FILING DATE: 2000-07-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-24

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-10-02-24

PRIOR FILING DATE: 1999-00-02-24

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-08-08

PRIOR PRIOR PRICE TOWN NUMBER: US 60/146,002

PRIOR PRIOR PRICE TOWN NUMBER: US 60/146,002
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Best Local Similarity 54.5%; Pred. No. 3.3;
Matches 79; Conservative 0; Mismatches 66;
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                                                                                                                                                                                                                                                                                                                                             126 AGAGAGATGCCGATGAAGAAGAAGAGATGATCTCGAAGAAAGGGATGTTGAAGTGGAAA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 116, Application US/10411910A
Publication No. US20040209256A1
GENERAL INFORMATION:
APPLICANT: Dillon, Harrison F.
TITLE OF INVENTION: Methods and Compositions for Evolving Hydrogenase Genes
FILE REFERENCE: H2441203-P
CURRENT APPLICATION NUMBER: US/10/411,910A
CURRENT FILING DATE: 2003-04-12
NUMBER OF SEQ ID NOS: 343
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1509 CTGTATAATGGGTGGAGGACAGCCAATCCACAATCCTAACGAGATGGAAGAAGTAGAA 1568
                                                                                                                                                                                                                                                                                                                                                                                  186 AGCGATITITICCAGTGATIGGAAGGATACTCAATGGTATTTTTGGGAAAATAACCAAAAA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                               808 TAGAATTATATAAAGTTATTAAATATATATATATAGATATTTTGAGGGAGAGAAAAA 867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 TGGTATTTTGGGAAAATAACCAAAAAAGTTAAAACTTTGGAAATGGAATTGGAAATCAT 279
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                                                                                                                                                                                                           ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                          Length 8781;
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                                                                                                                                                                                                                                                                                                             86; Indels
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                                                                                                                                                                                                                                                                      Score 39.4; DB 15;
Pred. No. 9.6;
0; Mismatches 86;
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Pred. No. 6.6;
0; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Thermoanaerobacter tengcongensis
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 51.4%;
Matches 91; Conservative
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ilarity 51.8%;
Conservative
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Best Local Similarity
Matches 88; Conserv
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LENGTH: 1746
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/664,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 AAGAGATGATCTCGAAGAAAGGGATGTTGAAGTGGAAAAGCGATTTTTTCCAGTGATTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 Arcrergarrrrerarraaaacrrrreragacreaagaaar 190
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.63
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Pred. No. 4;
0; Mismatches
                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-08-03
PRIOR PLICATION NUMBER: US 09/632,366
PRIOR PLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PRILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/US01/00667
PRIOR PRILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR FILING DATE: 2001-01-01
PRIOR FILING DATE: 2001-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 16328
LENGTH: 466
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Best Local Similarity 52.1%;
Matches 86; Conservative (
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RESULT 13 US-10-424-599-44115

Sequence 16328, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION: APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.

RESULT 12 US-09-864-761-16328

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                                               APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Exercise Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwel
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRESENCE: 38-21 (53223)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 44115
LENGTH: 2211
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; Sequence 3, Application US/09982091A
; Patent No. US20020151030A1
; GENERAL INFORMATION:
    APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
; APPLICANT: CUNFRY, William
; TITLE OF INVENTION: CLASPIN PROTEINS AND METHODS OF USE THEREOF
; PILE REFERENCE: CIT1320-1
; CURRENT APPLICATION NUMBER: US/09/982,091A
; CURRENT PILING DATE: 2002-10-17
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NOS: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2211;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   11.7%; Score 38.6; DB 17;
55.6%; Pred. No. 8.3;
iive 0; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT3847_139834C.1
US-10-424-599-44115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 11.7%; Score 38.6; DB Best Local Similarity 53.7%; Pred. No. 12; Matches 80; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 CAAAAAAGTTAAAACTTTGGAAATGGAA 268
Sequence 44115, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
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Best Local Similarity 55.6'
Matches 74; Conservative
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                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Glycine max
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                                                                                                                                         ; Sequence 777, Application US/09764860
; Batent No. US2002094953A1
; GENERAL INFORMATION:
; APPLICATT: Rosen et al.
; TILLE OF INVENTION: NUCLEIC Acids, Proteins, and Antibodies
; TILLE REFERENCE: PC008
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT APPLICATION ACIDES: US/09/764,860
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT APPLICATION NUMBER: US/09/764,860
; VINDER OF SEQ ID NOS: 1198
; SEQ ID NO 777
; ENGTH: 23934
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11.7%; Score 38.6; DB 9;
Best Local Similarity 47.3%; Pred. No. 25;
Matches 116; Conservative 0; Mismatches 129;
2146 CAAAAGATGAAAAGAAATGGATAAAGAA 2174
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; LOCATION: (53)..(235)
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Sequence 16. Appl
Sequence 1, Appl
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Sequence 17010, A
Sequence 4455, Ap
Sequence 13877, Ap
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Sequence 1, Appli
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Sequence 15, Appl
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/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-936-885A-15
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US-09-940-016-17010
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US-09-680-726A-1
US-09-092-409-1
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Sequence 51, Appl
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Sequence 979, Ap
Sequence 16267, A
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Sequence 15492, A
Sequence 15492, A
Sequence 16492, A
Sequence 17012, A
Sequence 17012, A
Sequence 17 Appl
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Sequence 17 Appl
Sequence 1, Appli
US-09-092-409-51

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US-09-248-796A-9079

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US-09-949-016-13766

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US-09-128-155-17

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US-09-128-155-17

US-09-969-155-17

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CCCCTCCAGCTGTCTACATTCTCATAACCAACCACACCCCCAGCCCCAAAGATGTTCAC GGAAGAGAGATGCCGATGAAGAAGAAGAGATGTCTCGAAGAAAGGGATGTTGAAGT GGAAAAGCGATTTTTTCCAGTGATTGGAAGGATACTCAATGGTATTTTGGGAAAATAACC GGAAAAGCGATTTTTTCCAGTGATTCGAAGGATACTCAATGGTATTTTGGGAAAATAACC CCCCTCCAGCTGTCTATATCTCATAACCAACTGAACCACCCGAGCCCAAAGATGTTCAC ; 0 100.0%; Score 329; DB 3; Length 329; llarity 100.0%; Pred. No. 8.7e-80; Conservative 0; Mismatches 0; Indels USCOULT 19-730-18

1 Sequence 18, Application US/09319730

2 Patent No. 6310176

3 GENERAL INFORMATION:

4 APPLICANT: SIMMACO, MAURIZIO

5 TITLE OF INVENTION: ANTIMICROBIALLY ACTIVE POLYPEPTIDES

7 TITLE REFERENCE: 003300-574

6 CURRENT APPLICATION NUMBER: US/09/319,730

7 CURRENT APPLICATION NUMBER: US/09/319,730

7 CURRENT FILING DATE: 1999-08-24

7 PRIOR APPLICATION NUMBER: SE 9604593-5

7 PRIOR FILING DATE: 1996-12-12

7 PRIOR FILING DATE: 1996-12-13

7 NUMBER OF SEQ ID NOS: 19

7 SEQ ID NOS: 19

7 SEQ ID NOS: 19 TYPE: DNA ORGANISM: Rana Temporaria FEATURE:

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61.9%; Score 203.8; DB 3; Length 356;
Best Local Similarity 81.7%; Pred. No. 7.9e-46;
Matches 267; Conservative 0; Mismatches 42; Indels 18
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Sequence 16, Application US/09319730

Sequence 16, Application US/09319730

Patent No. 631016

GENERAL INFORMATION:

APPLICANT: SIWARO, MAURIZIO

TITLE OF INVENTION: ANTIMICROBIALLY ACTIVE POLYPEPTIDES

TITLE OF INVENTION: 1999-574

CURRENT PILING DATE: 1999-68-24

CURRENT FILING DATE: 1999-68-24

PRIOR FILING DATE: 1997-12-12

PRIOR FILING DATE: 1997-12-12

PRIOR PLING DATE: 1997-12-12

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PatentIn Ver. 2.0
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PRIOR APPLICATION NUMBER: SE 9604593-5
PRIOR FILING DATE: 1996-12-13
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Rana Temporaria
                                                                                                                                                                                                                            ORGANISM: Rana Temporaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            322 TATAAAA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297 TATTTAAA 304
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; LOCATION: (79)..(252)
US-09-319-730-16
                                                                                                                                                                                                                                                                FEATURE:

NAME/KEY: CDS

LOCATION: (37)..(219)
US-09-319-730-14
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                                                                                                                                                                                                     TYPE: DNA
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                                                                                                                                                                                                        US-09-936-885A-15

Sequence 15, Application US/09936885A

Sequence 15, Application US/09936885A

Sequence 15, Application G83868

GENERAL INFORMATION:

APPLICANT: Mista and Kay

TITLE OF INVENTION: Trangenic Plants that are Resistant to a Broad Spectrum

TITLE OF INVENTION: OF PAthogens

FILE REFERENCE: 60993

CURRENT PELING DATE: 2001-09-17

PRIOR PILING DATE: 1999-03-17

PRIOR PLING DATE: 1999-03-17

PRIOR PLING DATE: 1000-03-16

NUMBER OF SEQ ID NOS: 42

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 15

LENGTH: 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CCCCTCCAGCTGTCTACATTCTCATAACCAACTGAACCACCCGAGCCCAAAGATGTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 cricaacaaarcccrcrracrccrrrrcrrccrrccaccarcaacrrarcrcrcrcrc
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100.0%; Score 329; DB 4; Length 329;
Best Local Similarity 100.0%; Pred. No. 8.7e-80;
Matches 329; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/09319730
Patent No. 6310176
Patent No. 6310176
Patent No. 6310176
Patent No. 6310176
APPLICANT: SIMMACO, Maurizio
APPLICANT: SIMMACO, Maurizio
APPLICANT: SIMMACO, ANTIMICROBIALLY ACTIVE POLYPEPTIDES
FILE REFERENCE: 003300-574
CURRENT APPLICATION NUMBER: US/09/319,730
PRIOR APPLICATION NUMBER: PGT/SE97/02075
PRIOR PAILNG DATE: 1997-12-12
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                   TYPE: DNA
ORGANISM: Rana temporaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: (53)..(238)
US-09-936-885A-15
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US-09-319-730-14
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Patent No. 6835868

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE O
                                                                                                     63 TGAAGAAATCCCTCTTACTCCTTTCCTTGGGACCATCAACTTATCTCTGTGAGG 122
                                                                                                                                                                                                                                                                                               AAGAGAAAATGCAGAAAGAAAGAAAGAGAGATGAACCAGATGAAAGGGGATGTTCAAGTGG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                209 AAAAACGACTITCACC-----AAACCIGCICAAGAGCITGITGGGAAAATAACCA- 258
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                                                                                                                                                                                                                                                                                                                                                                                         183 AAAAGCGATTTTTTCCAGTGATTGGAAGGATACTCAATGGTATTTTGGGAAAATAACCAA 242
                                                                                                                                                                                                                                               123 AAGAGAGAGATGCCGATGAAGAAAGAAGAGATGATCTCGAAGAAAGGGATGTTGAAGTGG 182
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; Pred. No. 0.0096;
· 0; Mismatches 35
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Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: P. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303 AAATGCACATCAAATGTCTTATAAAA 329
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Best Local Similarity 65.3*
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; LOCATION: (58)..(294)
US-09-936-885A-1
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US-08-232-463-14/c
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Sequence 17010, Application US/09949016

Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: PUTH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PLING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PLING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 GAGGAAGAGAGAGATGCCGATGAAGAAGAAGAGGATGTCTCGAAGAAAGGGGATGTTGAA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 GTGGAAAAGCGATTTTTCCAGTGATTGGAAGGATACTCAATGGTATTTTGGGAAAATAA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 CCAAAAAAGTTAAAACTTTGGAAATTGGAAATCGATCTAATGTGGAATGTCA 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 7218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
APPLICATION NUMBER: EF 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 39,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
12.3%; Score 40.6; DB
Best Local Similarity 2.3%; Pred. No. 0.39;
Matches 4; Conservative 117; Mismatches
                           E: Foley & Lardner
1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                      ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (703) 683-4109
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & I
STREET: 1800 Diagona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLONE: pTZgpt-Fl8
US-08-232-463-14
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                                                                     Alexandria
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                                                                                                                    USA
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                                                                                                                    COUNTRY:
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US-09-949-016-183626
                                                    US-09-949-016-13877/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Human
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Squence 4455, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TILE REFERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR PAPLICATION NUMBER: 60/241,755

PRIOR PAPLICATION NUMBER: 60/241,755

PRIOR PAPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FESTSEQ for Windows Version 4.0

SEQ ID NO 4455

LENGTH: 4756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           34849 TAĞTAAAAATATTTCTAĞATTTTTĞAAĞAAĞATAAGCATTAAAATAATTAĞTATĞAAĞA 34790
                                                                                                                                                                                                                                                                                                                                                                              34909 ATACAAATGATGAGTAGCAATATCTAGTGGCTCATGTGAAAGCAACTTTTTTTCAGCTT 34850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 AGGAAGAGAGAGATGCCGATGAAGAAGAAGAGATGATCTCGAAGAAAGGGATGTTGAAG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 IGGAAAAGCGAITTTTCCAGTGATTGGAAGGATACTCAATGGTATTTTGGGAAAATAAC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 IGGAATIGGAAAICAICIAAIGIGGAAIGICAITIAGCIAAAIGCACAICAAAIGICIIA 323
                                                                                                                                                                                                                                                                                                                                                                                                                      144 AAAGAAGATGATCTCGAAGAAAAGGGATGTTGAAGTGGAAAAAGCGATTTTTTCCAGTGA 203
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                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 51.4%; Pred. No. 0.72;
Matches 94; Conservative 0; Mismatches 89; Indels 0;
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12.2%; Score 40.2; DB
Best Local Similarity 54.4%; Pred. No. 0.43;
Matches 81; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2150 CAAAAGATGAAAAGAAATGGATAAAGAA 2178
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NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17010
LENGTH: 45983
                                                                                                                                                      ; NAME/KEY: misc_feature
; LOCATION: (1)...(45983)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17010
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ORGANISM: Human
                                                                                            TYPE: DNA
ORGANISM: Human
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Sequence 11877, 6 681239

Sequence 11877, 6 681239

GENERAL INFORMATION: Cris of all the properties of the control of the cont
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LOCATION: (559167)..(559167)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (559241)..(559241)
OTHER INFORMATION: n equals a, t,
                                                                  NAME/KEY: misc_feature
LOCATION: (191989). (191989)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc_feature
LOCATION: (191995)..(191995)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc_feature
LOCATION: (231980)..(231980)
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LOCATION: (234220). (234220)
CTHER INFORMATION: n equals a, t.
NAME/KEY: misc_feature
LOCATION: (234814)..(234814)
OTHER INFORMATION: n equals a, t.
NAME/KEY: misc_feature
LOCATION: (309398)
OTHER INFORMATION: n equals a, t.
                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (234187) ..(234187)
OTHER INFORMATION: n equals a,
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THER INFORMATION: n equals a,
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LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals a,
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LOCATION: (312837)..(312837)
OTHER INFORMATION: n equals a,
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LOCATION: (312993)..(312993)
OTHER INFORMATION: n equals a,
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LOCATION: (674435)..(674435)
OTHER INFORMATION: n equals a,
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LOCATION: (309418)..(309418)
OTHER INFORMATION: n equals a,
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LOCATION: (600992)..(600992)
OTHER INFORMATION: n equals a,
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LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals a,
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LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a,
                              ION: (163385)..(163385)
INFORMATION: n equals a,
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LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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LOCATION: (713\overline{652})..(713\overline{652})
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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sequence 1, Application US/09692570

Patent No. 6797466

GENERAL INFORMATION:
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococc;
TITLE OF INVENTION: jannaschii
Patent No. 6797466

TITLE OF INVENTION: jannaschii
PILE REPERENCE: PE375C1

CURRENT APPLICATION NUMBER: US/09/692,570

CURRENT APPLICATION NUMBER: US 60/024,428

PRIOR APPLICATION NUMBER: US 08/916,421

PRIOR APPLICATION NUMBER: US 08/916,421

PRIOR APPLICATION NUMBER: US 08/916,421

PRIOR FILING DATE: 1996-08-22

PRIOR FILING DATE: 1997-08-22

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 1564976
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LOCATION: (163385)..(163385)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Methanococcus jannaschii
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LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals a,
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LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a,
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LOCATION: (98343)...(98343)
OTHER INFORMATION: n equals a,
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LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a,
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LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a,
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LOCATION: (103998)..(103998)
OTHER INFORMATION: n equals
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LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals
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LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals
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LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals
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LOCATION: (98239)..(98239)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals
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LOCATION: (28222)..(28
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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Best Local Similarity 50.5%; Pred. No. 5.8;
Matches 95; Conservative 0; Mismatches 93; Indels 0;
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LOCATION: (1664854)..(1664855)
OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (1637998)..(1637998)
OTHER INFORMATION: n equals a, t,
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LOCATION: (1349491)..(1349491)
OTHER INFORMATION: n equals a, t,
                                                                        LOCATION: (855539). (855539)
OTHER INFORMATION: n equals a, t, omans/KEY: misc_feature
LOCATION: (871619). (871619)
OTHER INFORMATION: n equals a, t,
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IION: (1313224)..(1313224)
R INFORMATION: n equals a, t,
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LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
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THER INFORMATION: n equals a, t,
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LOCATION: (1602912)..(1602912)
OTHER INFORMATION: n equals a, t.
NAME/KEY: misc feature
LOCATION: (1603734)..(1603734)
OTHER INFORMATION: n equals a, t.
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OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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LOCATION: (1349473)..(1349473)
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US-09-692-570-1/c
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LOCATION: (674435)..(674435)
JTHER INFORMATION: n equals a, t, c, or g
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NAME/KEY: misc_feature
LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc feature
LOCATION: (234220)..(234220)
OTHER INFORMATION: n equals a, t,
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LOCATION: (234814)..(234814)
OTHER INFORMATION: n equals a, t,
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LOCATION: (312837)..(312837)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (191989)..(191989)
OTHER INFORMATION: n equals a, t,
                                                                       NAME/KEY: misc feature
LOCATION: (191995)..(191995)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc_feature
LOCATION: (319226)..(319226)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc_feature
LOCATION: (559241)..(559241)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc_feature
LOCATION: (600992)..(600992)
OTHER INFORMATION: n equals a, t,
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LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a, t,
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LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a, t,
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LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals a, t,
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NAME/KEX: misc_feature
LOCATION: (234187)..(234187)
OTHER INFORMATION: n equals a,
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LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals a,
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LOCATION: (309418)..(309418)
OTHER INFORMATION: n equals a,
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LOCATION: (312993)..(312993)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc_feature
LOCATION: (559167)..(559167)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t, c, or g
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NAME/KEY: misc_feature
LOCATION: (1313224). (1313224)
OTHER INFORMATION: n equals a, t, c, or
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NAME/KEY: misc_feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a, t, c,
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LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a, t,
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LOCATION: (871519)..(871619)
OTHER INFORMATION: n equals a, t,
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LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a, t,
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LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a, t,
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LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a, t,
LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals a,
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LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a,
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LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a,
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LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a,
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LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals
                                                     NAME/KEY: misc feature
LOCATION: (713552)...(713552)
OTHER INFORMATION: n equals
FEATURE:
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Best Local Similarity 50.58
Matches 95; Conservative
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RESULT 15
US-08-602-010A-5/c
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                                                                        Sequence 2. Application US/07867106

Facent No. 5389526

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Slade, Martin B

APPLICANT: Williams, Keith L

TITLE OF INVENTION: Improved Plasmid Vectors for Cellular

TITLE OF INVENTION: Slime Moulds of the Genus Dictyostellum

NUMBER OF SEQUENCES: 19

CORRESPONDENCE 3. 19

STREET: One Liberty Place 46th Floor

CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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Best Local Similarity 52.2%; Pred. No. 2.1;
Matches 84; Conservative 0; Mismatches 77; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

CORRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/867,106

FILING DATE: 19920625

PRIOR APPLICATION NUMBER: PCT/AU90/00530

PTLING DATE: ON-NOV-1989

ATTORNEY/AGENT INFORMATION:

NAME: PEERENCE/POCKET UNBER: 35,134

REGISTRATION NUMBER: 35,134

REGISTRATION NUMBER: 35,134

RELEPAN: 215-568-3100

TELLEPAN: 215-568-3100

TELLEPAN: 215-568-3109

INFORMATION FOR SEQ 1D NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: SES Dase pairs

LENGTH: SES Dase pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
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2378..5038
1641709 TTAGAGAA 1641702
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2378..5038
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FEATURE:
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FEATURE:
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, LOCATION:
US-07-867-106-2
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                                                           RESULT 13
US-07-867-106-2
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279416 AAAAATTTAATTTTTTAGAATACAACTAAAAAGAATCTGAAGAAAAAATAATAGAA 279475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 AAGCGAITTTTCCAGTGATTGGAAGGATACTCAATGGTATTTTGGGAAAATAACCAAAA
US-09-790-988-1
Sequence 1, Application US/09790988
Sequence 1, Application US/09790988
Sequence 1, Application US/09790988
Sequence 1, Application US/09790988
Septicant: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: MATANABE, HIDEMI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
TITLE OF INVENTION: GENOME DNA OF US/09/790, 988
CURRENT APPLICATION NUMBER: US/09/790, 988
CURRENT APPLICATION NUMBER: J2001-02-23
PRIOR APPLICATION NUMBER: J2001-02-23
PRIOR PILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
11.4%; Score 37.4; DB 4; Length 640681;
Best Local Similarity 51.5%; Pred. No. 13;
Matches 86; Conservative 0; Mismatches 81; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 AAAGTTAAAACTTTGGAAATGGAATTGGAAATCATCTAATGTGGAAT 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5. Application US/08602010A
Patent No. 575325
GENERAL INFORMATION:
APPLICANT: Hannes, Elizabeth J.
APPLICANT: Frank, Rexann S.
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSER: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Sulte 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,010A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: February 15, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CORDIJ, GARY J.
REGISTRATION NUMBER: 32,020
REFFERENCE/DOCKET NUMBER: 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-9700
                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 640681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Buchnera sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Denver
STATE: Colorado
COUNTRY: U.S.A
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1176 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FALTURE:
; NAME/KEY: CDS
; LCCATION: 1..1176
US-08-602-010A-5

Query Match
Best Local Similarity 58.0%; Pred. No. 2.2;
Matches 65; Conservative 0; Mismatches 47; Indels 0;
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Search completed: March 31, 2005, 18:26:04 Job time : 105 secs THIS PAGE BLANK (USPTO)

OM nucleic

Run on:

Sequence:

Title:

Searched:

Database

Result

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Y16565 Phyllomedus
X72387 P. Dicolor m
BD56888 Transgeni
BC048586 Mus muscu
AC112564 Rattus no
AY11879 Litoria c
AY218779 Litoria c
        AJ54406 Codorrana
AJ427748 Rana pipi
U22392 Rana rugosa
AJ21156 Rana rugosa
AZ218784 Phyllomed
AJ318759 Kassina s
AJ54792 Phyllomed
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Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Temporins, antimicrobial peptides from the European red frog Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (11-NOV-1996) D. Barra, Universita La Sapienza,
Dipartimento Di Scienze Biochimiche, Piazzale Aldo Moro 5, 00185
Roma, ITALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Simmaco, M., Mignogna, G., Canofeni, S., Miele, R., Mangoni, M.L. and
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/cvidence=xperimental
/product="temporin G precursor"
/protein_id="CAA70564.1"
/db_xref="G1.771592"
/db_xref="G0A:1771892"
/db_xref="UniProt/Swiss-Prot:P79875"
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R.temporaria mRNA for temporin G precursor.
Y09395
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53. .238
/function="antibacterial activity"
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KSE318759
PSA549500
PSA564792
PSA564791
ACL131876
AAAJ5188
PDA507318
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AAAJ5186
PBY16566
PBY16565
PBDERSPB
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Rana temporaria
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Y09395.1 GI:1771591
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RTTEMPORG
LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE
PUBMED
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υ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARITGO40 Sequence
BD268889 Transgeni
BD063212 Antimicro
S69903 Ranalexin=a
Y09393 R.temporari
ARIT6038 Sequence
BD065210 Antimicro
Y09394 R.temporari
ARIT6039 Sequence
BD065211 Antimicro
X77831 R.esculenta
UZ2393 Rana rugosa
AJ47746 Rana pipi
AJ47747 Rana pipi
AJ427747 Rana pipi
AJ427747 Rana pipi
AJ427747 Rana pipi
AJ583666 Rana temp
                                                                                                     March 31, 2005, 14:45:33 ; Search time 1389 Seconds (without alignments) 11477.153 Million cell updates/sec
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                                                                                                                                                                                                     1 ccctccagctgtctacatt........atcaaatgtcttataaaaa 329
                                                                                                                                                                                                                                                                                                                    9416466
              GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                   4708233 segs, 24227607955 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                            nucleic search, using sw model
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BD268889
BD063212
BD063212
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RTTEMPORB
AR176038
RTTEMPORH
AR176039
BD063211
REBRELE
RRU2393
RP1427745
AJ583866
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RTE251567
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                                                                                                                                                                     US-10-719-623A-15
329
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Maximum DB seq length: 200000000
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Match Length
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VRT 02-OCT-2003

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329 bp DNA linear PAT 17-JUL-2003
Transgenic plant having tolerance to wide-area pathogen.
BD268889
BD2688891 GI:33078657
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PI SANTOSH MISBA, WILLIAM W KAY
9C A01H5/00, C07K14/415//C12N5/10, C12N15/09, C12N15/00, C12N5/00 CC
Transgenic plant having tolerance to wide-area pathogen FH Key
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
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AAAAAAAGTTAAAAACTTTGGAAATGGAATTGGAAATCATCTAATGTGGAATGTCATTTAG 300
                                                                                                                                                      241 AAAAAAAGTTAAAAACTTTGGAAATGGAAATTGGAAATCATCTAATGTGGAATGTCATTTAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                               Rana temporaria
Rana temporaria
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAAAAAGTTAAAAACTTTGGAAATGGAATTGGAAATCATCTAATGTGGAATGTCATTTAG 300
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Misra, S. and Kay, W.W.

Transgenic plant having tolerance to wide-area pathogen

Transgenic plant having tolerance to wide-area pathogen

Divided to 200253828-A 2 19-NOV-2002;

NIVERSITY OF VICTORIA INNOVATION AND DEVELOPMENT CORP

OS Rana temporaria (european common frog)

PD 19-NOV-2002

PP 16-MAR-2000 JP 2000605754

PR 17-MAR-1999 US 60/125072

PI SANTOSH MISRA, WILLIAM W KAY

PC A01H5/00, CO7K14/415//C12N5/10, C12N15/09, C12N15/00. C12N15
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100.0%; Pred. No. 1.6e-65;
iive 0; Mismatches 0;
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/organism="Rana temporaria"
/mol_type="genomic DNA"
/db xref="taxon:8407"
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Location/Qualifiers
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 /translation="MPTLKKSLLLLFFLGTINLSLCEERDADEERRDDLEERDVEVE
KRFPPVIGRILNGILGK"
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241 AAAAAAAGTTAAAACTTTGGAAATGGAATTGGAAATCATCTAATGTGGAATGTCATTTAG 300
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llarity 100.0%; Pred. No. 1.6e-65;
Conservative 0; Mismatchea
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1 (bases 1 to 329)

1 sares, D. and Simmaco, M.

Antimicrobially active polypeptides

Patent: US 6310176-A 18 30-OCT-2001;

Location/Qualifiers
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Sequence 18 from patent US 6310176.
AR176040.1 GI:17917339
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                                                           /evidence=not_experimental
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/product="Ranalexin"
/protein_id="AAB30394.1"
/bxref="qi:546212"
/rranslation="MTLIKKSLLLFFLGTINLSLCEEERNAEEERRDNPDERDVEVE
KRFLGGLIXIVPAMICAVTKKC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="antimicrobial peptide polymyxin homolog; precursor;
Method: conceptual translation with partial peptide
869903 347 bp mRNA linear VRT 23-SEP-1994
Ranalexin=antimicrobial peptide polymyxin homolog [Rana
catesbeiana=bullfrogs, metamorphic tadpoles, skin cells, mRNA, 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 TGAAGAAATCCCTGTTACTCCTTTTCTTCCTTGGGACCATCAACTTATCTCTCTGTGAGG 121
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                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana;
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                                                                                                                                                                                                                                                                                                                                                                                                 GenBank staff at the National Library of Medicine created this entry (NCBI gibbsg 146812) from the original journal article.
Location/Qualifiers
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                                                                                                                                                                                                                                                      Clark, D.P., Durell, S., Maloy, W.L. and Zasloff, M. Ranalexin. A novel antimicrobial peptide from bullfrog (Fcatesbeiana) skin, structurally related to the bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 347;
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J. Biol. Chem. 269 (14), 10849-10855 (1994)
94193792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .347
/organism="Rana catesbeiana"
/mol_type="mRNA"
/db_xref="taxon:8400"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="Ranalexin"
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S69903.1 GI:546211
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Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana;
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100.0%; Pred. No. 1.6e-65;
tive 0; Mismatches 0;
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1 (Bases 1 to 329)

Barra, D. and Simmaco, M.

Antimicrobially active polypeptides
Patent: JP 2001506495-A 3 22-MAY-2001;
SBL VACCIN AB
OS Rana temporaria
PN JP 2001506495-A/3
PP 12-DEC-1997 JP 1998526559
PR 13-DEC-1996 SE 9604593-5
PI DONNATELA BARRA, MAURIZIO SIMMACO
CC CONA clone Rt-17
FH Key
FT COS (C338)
FT COS (191) (229)
FT polyA signal (323) (327).
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                                                                                                                                                                 Antimicrobially active polypeptides.
BD063212
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/organism="Rana temporaria"
/mol_type="genomic DNA"
/db_xref="taxon:8407"
                  CTAAATGCACATCAAATGTCTTATAAAA 329
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Rana temporaria
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Location/Qualifiers
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JP 2001506495-A/3.
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66 CCTCTTTTCCTTGGGACCATCAACTTATCTCTGTGAGGAGAAGAGAAATGCAGAAGA 125
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Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana,
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Unclassified.

E 1 (bases 1 to 323)
S Barra,D. and Simmaco,M.
Antimicrobially active polypeptides
Antimicrobially active polypeptides
[AL Patent: US 6310176-A 14 30-OCT-2001;
Location/Qualifiers
123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 64.7%; Score 212.8; DB 6 Best Local Similarity 83.4%; Pred. No. 9.1e-39; Matches 257; Conservative 0; Mismatches 42
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Antimicrobially active polypeptides.
BD063210 GI:22608813
JP 2001506495-A/1.
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Barra, D. and Simmaco, M.
Antimicrobially active polypeptides
Patent: JP 2001506495-A 1 22-MAY-2001;
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Sequence 14 from patent US 6310176.
AR176038
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/organism="unknown"
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Rana temporaria
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297 TATTTAAA 304
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                                                     322 TATAAAA
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/translation="MFTLKKSLLLLFFLGTINLSLCEEERNAEEERRDEPDERDVQVE
     VRT 02-OCT-2003
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Rana temporaria
Bukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibla; Batrachia; Anura; Neobatrachia; Ranoidea; Rana;
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                                                                                                                                                                                                                         Temporins, antimicrobial peptides from the European red frog Rana
                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (11-NOV-1996) D. Barra, Universita La Sapienza,
Dipartimento Di Scienze Biochimiche, Piazzale Aldo Moro 5, 00185
                                                                                                                                                                                    Simmaco, M., Mignogna, G., Canofeni, S., Miele, R., Mangoni, M.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17. .222
/function="antibacterial activity against gram-positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 TCTGAGCCAACTGAACCACCCGAGCCCAAAGATGTTCACCTTGAAGAAATCCCTGTTACT
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323 bp mRNA
R.temporaria mRNA for temporin B precursor.
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Best Local Similarity 83.4%; Pred. No. 9.1e-39;
Matches 257; Conservative 0; Mismatches 42
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modification"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Rana temporaria"
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/tisue type="skin"
/clone_lib="RT-5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=experimental 37. .103 /evidence=not_experimental
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temporin B.
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97175050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 TGAAGAAATCCCTCTTACTCCTTTTCTTCCTTGGGACCATCAACTTATCTCTCTGTGAGG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 AAAAGCGATTTTTCCAGTGATTGGAAGGATACTCAATGGTATTTTGGGAAAATAACCAA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209 AAAAAcGACTTTCACC-----AAACCTGCTCAAGAGCTTGTTGGGAAAATAACCA- 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 AAAAAGTTAAAACTTTGGAAATGGAATTGGAAATCATCTAATGTGGAATGTCATTTAGCT 302
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   Dipartimento Di Scienze Biochimiche, Piazzale Aldo Moro 5, 00185
Roma, ITALY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
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                                                          1. .356
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Best Local Similarity 81.7%; Pred. No. 1.1e-36;
Matches 267; Conservative 0; Mismatches 42
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1 (bases 1 to 356)

Barra,D. and Simmaco,M.
Antimicrobially active polypeptides
Patent: US 6310176-A 16 30-OCT-2001;
Location/Qualifiers
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AR176039.1 GI:17917338
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/evidence=experimental
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AR176039
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Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Simmaco, M., Mignogna, G., Canofeni, S., Miele, R., Mangoni, M.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGAAAGAAGAGATGATCTCGAAGAAAGGGATGTTGAAGTGGAAAAGCGATTTTTTCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 rcreaccaacreaaccaccaaccaaacarerrcaccrreaagaarcccrerracr
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Submitted (11-NOV-1996) D. Barra, Universita La Sapienza,
                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                   Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                       42; Indels
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97175050
                                                                                                                                                                                                                                                                                                                                                                             Score 212.8; DB 6
Pred, No. 9.1e-39;
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                                                                        12-DEC-1997 JP 1998526559
12-DEC-1996 SE 9664593-5
DONNATELLA BARRA, MAURIZIO SIMMACO
COTK14/46, COTK7/08, A61K33/56

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64.7%; Score 212.8; Best Local Similarity 83.4%; Pred. No. 9.1e
Matches 257; Conservative 0; Mismatches
                                                                                                                                                                                      CDS (37). .(222) mat peptide (175). .(213) polyA signal (307). .(311). Location/Qualifiers
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Rana temporaria
                   Rana temporaria
JP 2001506495-A/1
22-MAY-2001
                                                                                                                                                   cDNA clone Rt-5
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302

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/codon_start=1
/product="brevinin-1E precursor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   VRT 19-JUN-1996
                                                                 63 TGAAGAAATCCCTCTTACTCCTTTTCTTCCTTGGGACCATCAACTTATCTCTGTGAGG 122
                                                                                                                                                                                                                          209 AAAAAcaAchricacc-----AAAccrccrcaAaaGcrrcrigrragaAAAAAAAAAAA
                                                                                                                                                                                                                                                                            123 AAGAGAGAGATGCCGATGAAGAAAGAAGAGATGATCTCGAAGAAAAGGGATGTTGAAGTGG 182
                                                                                                                                                   Euteleostomi;
Ranidae; Rana;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (10-FEB-1994) M. Simmaco, Nodo Nazionale Italiano (area
di, ricerca CNR-Bari), Via Amendola 168/5, 70126 Bari, ITALY
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Simmaco,M., Mignogna,G., Barra,D. and Bossa,F.
Antimicrobial peptides from skin secretions of Rana esculenta.
Molecular cloning of cDNAs encoding esculentin and brevinins and
J. Biolation of new active peptides
J. Biol. Chem. 269 (16), 11956-11961 (1994)
                        29 CTTCCAGCCGTCTACATTCTGAGCACCAACTGAACTACCCGAGCCCAAAGATGTTCACCT
                                                                                     183 AAAAGCGATTTTTCCAGTGATTGGAAGGATACTCAATGGTATTTTGGGAAAATAACCAA
                                                                                                                                                                                                                                                          243 AAAAAGTTAAAACTTIGGAAATGGAAATCATCTAATGTGGAATGTCATTTAGCT
        CCTCCAGCTGTCTACATTCTCATAACCAACTGAACCACCGAGCCCAAAGATGTTCACCT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
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/mol type="mRNA"
/db_xref="taxon:8401"
/clone lib="skin"
57. 272
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R.esculenta mRNA for brevinin-1E.
X77831
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/product="brevinin-1E"
/evidence=experimental
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JP 2001506495-A/2.
Rana temporaria (common frog)
Rana temporaria
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Rana,
                                                                                                                                                                                                   63 TGAAGAAATCCCTCTTACTCCTTTCTTCCTTGGGACCATCAACTTATCTCTCTGTGAGG 122
                                                                                                                                                                                                                   89 TGAAGAAATCCCTGTTACTCCTCTTTTTCCTTGGGACCATCAACTTATCTCTCTGTGAGG 148
                                                                                                                                                                                                                                                               AAGAGAGAGATGCCGATGAAGAAAGAAGAGATGATCTCGAAGAAAGGGATGTTGAAGTGG 182
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                                                                                                                                                                                                                                                                                                                                                           209 AAAAACGACTTTCACC-----AAACCTGCTCAAGAGCTTGTTGGGAAAATAACCA- 258
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                                                                                                                                                      CTTCCAGCCGTCTACATTCTGAGCACCAACTGAACTACCCGAGCCCAAAGATGTTCACCT
                                                                                                                                      CCTCCAGCTGTCTACATTCTCATAACCAACTGAACCACCCGAGCCCAAAGATGTTCACCT
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                                                                                                       18;
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                                                                         Length 356;
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                                                                         DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rana temporaria
JP 2001506495-A/2
J2-MAY-2001
12-DEC-1997 JP 1998526559
13-DEC-1996 SE 9604593-5
DONNATELLA BARRA, MAURIZIO SIMMACO
COTXIA/46, COTXI/08, A61K33/56
CDNA clone Rt-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                        Score 203.8; DB 6
Pred. No. 1.1e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA
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Barra,D. and Simmaco,M.
Antimicrobially active polypeptides
Pacent: JP 2001506495-A 2 22-MAY-2001;
SBL VACCIN AB
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Location/Qualifiers
1...356
/organism="Rana temporaria"
/mol_type="genomic DNA"
/db_xref="taxon:8407"
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Antimicrobially active polypeptides.
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(217) . . (246)
(307) . . (311) .
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                                                                      Query Match 61.9%;
Best Local Similarity 81.7%;
Matches 267; Conservative
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/ function="antimicrobial"

/ function="antimicrobial"

/ product="brevinin 1Pb"

/ product="brevinin 1Pb"

/ product="CAD20745.1"

/ db_xref="GOA:080F0S"

/ db_xref="TOA:080F0S"

/ db_xref="TOA:080F0S"

/ db_xref="TOA:080F0S"

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                                                                                                                                                                                                                                                                                                                                 187 TAAGGTTCTGCCATCAGTTTTTTGTGCAATTACCAAAAAATGTTAAAAACTT-----A 238
                                                                                                                                                                                                                                                                                                                                                                                                                 239 AATIGGAAATCATTTGGAATATCATTCAGCTAAATGCACATCAGATGTCTTATAA 298
                                                                                                                                               147 GAAGAGATGATCTCGAAGAAGAAGTGTTGAAGTGGAAAAGCGATTTTTTCCAGTGATTG 206
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                                                                                                                                                                                                                                                                                                              266
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Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Farragher, S.M.
Direct Submission
Submitted (10-JAN-2002) Farragher S.M., School of Biomedical
Sciences, University of Ulster, Cromore Road, N. Ireland., UNITED
                                                                                                       68
                                                                                                 9 ACCAACTGAACTACCAGAACCCCAAAGATGTTCACCTTGAAGAAATCCTTGTTACTCCTTT
                                                                                                                                                                                                                                                                                                            207 GAAGGATACTCAATGGTATTTTGGGAAAATAACCAAAAAAAGTTAAAAACTTTGGAAATGG
                                                               27 ACCAACTGAACCACCGAGCCCAAAGATGTTCACCTTGAAGAAATCCCTCTTACTCCTTT
                         10;
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    Pred. No. 7.5e-28;
0; Mismatches 61;
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Rana pipiens (northern leopard frog)
Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        294 bp
Rana pipiens mRNA for brevinin 1Pb.
AJ427746
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2 (bases 1 to 294)
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      76.68;
    Best Local Similarity 76.6
Matches - 232; Conservative
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Location/Qualifiers
                                                                                                                                                                                                                                                 180 TGGAAAAGCGATTTTTCCAGTGATTGGAAGGATACTCAATGGTATTTTGGGAAAA--- 235
                                                                                                                                                                                                                                                                                                                                         187 TGGAAAAACGATTTCTTCCATTGTTGCCAGTCTGGCTGCTAATTTCTTGCCGAAAATAT 246
                                                                                                                                           63 TGAAGAAATCCCTCTTACTCCTTTCTTCCTTGGGACCATCAACTTATCTCTGTGAGG 122
                                                                                                                                                                                 67 IGAAGAAATCCAIGITACTCCTTTCTTCCTTGGGACCATCAACTTATCTCTGTGAGG 126
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Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana,
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                                                           3 CCTCCAGCTGTCTACATTCTCATAACCAACTGAACCACCCGAGGCCCAAAGATGTTCACCT
                         Gaps
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Molecular cloning of cDNAs encoding precursors of frog skin antimicrobial peptides from Rana rugosa
                       10;
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Pred. No. 7.5e-35;
0; Mismatches 57; Indels
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Rana rugosa gaegurin 5 cDNA, complete cds.
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302. .307
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                     Matches 270; Conservative
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Search completed: March 31, 2005, 17:57:26 Job time : 1392 Becs
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inhibitor."
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AJ414584
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peptide leucine arginine precursor.
Rana pipiens (northern leopard frog)
Rana pipiens (northern leopard frog)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana;
                                                                                                                                                                                CTCTGTGAGGAAGAGAGAGATGCCGATGAAGAAAGAAGAGATGATCTCGAAGAAAAGGGAT 172
                                                                                                                                                                                                                 64 TTCTGTGAGGAAGA---AAATGCAGAGGAAGAAGAATAGATGAGCCAGATGAAACGGAT 120
                                                                                                                                                                                                                                                     GTTGAAGTGGAAAAGCGATTTTTCCAGTGATTGGAAGGATA--------CTCA 218
                                                                                                                                                                                                                                                                                      121 GTTGAAGTGGAAAACGATTTTTACCAATTATTGCAGGCATAGCCGCTAAGGTCTTCCCG 180
                                                                                                                                                                                                                                                                                                                         219 ATGGTATTTTGGGAAAATAACCAAAAAAGTTAAAACTTTGGAAATGGAATTGGAAATCA 278
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Direct Submission
Submitted (17-SEP-2001) Farragher S., School of Biomedical
Sciences, University of Ulster, Cromore Road, Coleraine, Northern
Ireland, BTS2 18A, UNITED KINGDOM
Location/Qualifiers
                                                                                                                                         63
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                                                                                                                              4 AIGITCACCTIGAAIAAATICCTICTACTCCTITTCTTCCTTGGGACCATCAACTIAICT
                                                                        Gaps
                                                                      17;
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                                                                        Indels
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                                   Score 149.6; DB 5;
Pred. No. 3.2e-24;
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                                                                                                           53 ATGITCACCTIGAAGAAAICCCICTTACICCI
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                                   tch 45.5%; al Similarity 76.6%; 216; Conservative (
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183 AAAAGCGATTTTTCCAGTGATTGGAAGGATACTCAATGGTATTTTGGGAAAATAACCAA 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                          240 TGTTTTGTAAGAGGATAAAACATGAATTGGAAGTCATCTGATGTGGAATATCATTTGGCT 299
                                                                                                                                                                  63 TGAAGAAATCCCTCTTACTCCTTTCTTCCTTGGGACCATCAACTTATCTCTCTGTGAGG 122
                                                                                                                                                                                          123 AAGAGAGAGATGCCGATGAAGAAAGAAGAGATGATCTCGAAGAAAAAGGGATGTTGAAGTGG 182
                                                                                                          3 CCTCCAGCTGTCTACATTACCAACTGAACCACCCGAGCCCAAAGATGTTCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                     243 AAAAAGTTAAAACTTTGGAAATGGAATTGGAAATCATCTAATGTGGAATGTCATTTAGCT
                                         Gape
                                         19;
  Length 362;
                                         Indels
                                         96
  DB 5;
Score 125.4; DB 5
Pred. No. 1.2e-18;
0; Mismatches 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 AAATGCTAAATGTCTGATAAAAAAAA 326
38.1%;
Query Match 38.1
Best Local Similarity 64.8
Matches 212; Conservative
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March 31, 2005, 14:38:32; Search time 256 Seconds (without alignments) 7607.793 Million cell updates/sec
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329
1 ccctccagctgtctacatt......catcaaatgtcttataaaaa 329
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aav07449 Rana temp	Aaa75750 cDNA enco	Aav07447 Rana temp	Aav07448 Rana temp	Adr88892 Nucleotid	Aaa75749 cDNA enco	Abn77187 Human ORF	Adc30694 Human nov	Abv30199 Human pro	Aas46794 Tumour su	Abl33686 Human imm	Continuation (17 o	Aai36639 Probe: #53	Abk52611 DNA encod	Aak71442 Human imm	Aal36171 Human mus	Aal36179 Human mus	Aal04522 Human rep	Aas28343 Genomic s	Ab197446 Human tes
SUMMARIES	QI	AAV07449	AAA75750	AAV07447	AAV07448	3 ADR88892	AAA75749	ABN77187	0 ADC30694	ABV30199	AAS46794	ABL33686	AAV21209 16	AAI36639	ABK52611	AAK71442	AAL36171	AAL36179	AAL04522	AAS28343	ABL97446
	Nery Atch Length DB	329 2	329 3	323 2	356 2	341 1	443 3	403 6	4414 1	4804 5	56153 4	8781 6	64976 2	466 4	4755 6	23934 4	23934 4	23934 4	23934 4	23934 4	23934 4
de	Ouery	100.0	100.0	64.7	61.9	14.2	13.7	12.3	12.2	12.2	12.2	12.0	11.9	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7
	Score	329	329	212.8	203.8	46.8	45	40.6	40.2	40.2	40	39.4	39.2	38.6	38.6	38.6	38.6	38.6	38.6	38.6	38.6
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ABA19145 ABX59167 ABX59159 ADG41539	AU197313 ADJ29917 ADJ29909 ABL33257 ABK80955	ADN36595 AAQ11710 ADL13935 AAC38796 ABA92787_2 AAS68161_	ABL37759 ABL07145 ABL07144 ABL33538	AAS/5450 AAV86185 AAV66903 AAF26723 AAT75590 AAV66900
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ALIGNMENTS

Temporin G; anti-microbial property; anti-fungal property; ss. 53. .238 /*tag= a /product= "Temporin G peptide" Location/Qualifiers Rana temporaria temporin G cDNA. AAV07449 standard; cDNA; 329 BP. 97WO-SE002075. 96SE-00004593 53. .118 /*tag= b 191. .229 /*tag= c 323. .327 /*tag= d (first entry) (SBLV-) SBL VACCIN AB. Simmaco M; WPI; 1998-362423/31. P-PSDB; AAW51843. Rana temporaria. WO9825961-A1. 12-DEC-1997; 13-DEC-1996; 26-OCT-1998 polyA_signal 18-JUN-1998 sig_peptide mat_peptide AAV07449; Barra.D, Key

Peptides from the skin of the frog Rana temporaria - useful as anti-microbial or anti-fungal compositions.

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Location/Qualifiers
                                                                                                    Disclosure; Page 49; 58pp; English.
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307. .311
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Best Local Similarity 100.
Matches 329; Conservative
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                                     The present sequence represents the Rana temporaria temporin G cDNA isolated from a R. temporaria skin cDNA library. The cDNA encodes a temporin G peptide which has anti-microbial properties. The invention claims for other R. temporaria derived peptides which are claimed to beeful in medicaments for anti-microbial and anti-fungal use
                                                                                                                                                                                                                                                                                                                                           CCCCTCCAGCTGTCTACATTCTCATAACCAACTGAACCACCCGAGCCCCAAAGATGTTCAC
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                                                                                                                                                                    Sequence 329 BP; 114 A; 62 C; 65 G; 88 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA encoding a temporin G precursor polypeptide
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/product= "temporin"
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53. .238
11; Page 19; 27pp; English
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The present sequence encodes a temporin precursor polypeptide. The specification also describes dermaseptin polypeptides. Temporin and dermaseptin have antibacterial activity. Dermaseptin also inhibits fungal growth. Cationic peptides derived from temporins and dermaseptins are used to produce transgenic plants. The transgenic plants are useful for producing biologically active cationic peptides such as temporins and dermaseptins in large quantities. The peptide confers broad spectrum pathogen resistance including enhanced resistance to both fungal and bacterial pathogens in the transgenic plants. The transgenic plants may be used in conventional agricultural applications such as food crops, medical and other applications
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Transgenic plants resistant to broad spectrum of pathogens useful for producing biologically active cationic peptides, comprises nucleic acid molecule encoding temporin and/or dermaseptin peptides.
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100.0%; Pred. No. 3.5e-80;
tive 0; Mismatches 0;
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66 CCTCTTTTTCCTTGGGACCATCAACTTATCTCTCTGTGAGGAAGAGAGAAATGCAGAAGA 125
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                                                                                                                                                                                                                         Peptides from the skin of the frog Rana temporaria - useful as anti-
microbial or anti-fungal compositions.
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                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 64.7%; Score 212.8; DB 2; Length 323; Best Local Similarity 83.4%; Pred. No. 2.6e-48; Matches 257; Conservative 0; Mismatches 42; Indels 9
                                                                                                                                                                                                                                                                                                                                                                            Sequence 323 BP; 119 A; 57 C; 64 G; 83 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                   Claim 11; Page 18; 27pp; English
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P-PSDB; AAW51841.
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                                                   18-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 AAAAGCGATTTTTCCAGTGATTGGAAGGATACTCAATGGTATTTTGGGAAAATAACCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            259 -----AAAATGTTAAGAATGGAATTGGAAATCATCTGATGTGGAATATCATTTAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 CCTCCAGCTGTCTACATTCTCATAACCAACTGAACCACCCGAGCCCCAAAGATGTTCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                         Peptides from the skin of the frog Rana temporaria - useful as anti-
microbial or anti-fungal compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 356 BP; 124 A; 69 C; 72 G; 91 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 61.9%; Score 203.8; DB 2; Best Local Similarity 81.7%; Pred. No. 7.8e-46; Matches 267; Conservative 0; Mismatches 42;
                                           "Temporin H peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311 AAATGCGCAACAGATGTCTTATTAAA 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 AAATGCACATCAAATGTCTTATAAAA 329
Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 18; 27pp; English.
                                                                                                                                                                                                                                                        96SE-00004593
                                                                                                                                                                                                                          97WO-SE002075
                            /*tag= a
/product=
79. 144
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339. 344
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                                                                                                                                                                                                                                                                                    (SBLV-) SBL VACCIN AB
                                                                                                                                                                                                                                                                                                                   Simmaco M;
                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-362423/31.
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                                                                                                                                                                                                                          12-DEC-1997;
                                                                                                                                                                                                                                                        13-DEC-1996;
                                                                                                                                                               409825961-A1
                                                                                                                     polyA_signal
                                                           sig_peptide
                                                                                       mat_peptide
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ADR88892 standard; cDNA; 341

ADR88892

ADR88892

vasodilatory; frog;

"tryptophyllin-1"

/product= 55. .114 55. .114 /*tag= a 115. .240 /*tag= c

Location/Qualifiers 55. .243

Ω

/*tag=

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The present sequence encodes a full length tryptophyllin-1, derived from Pachymedusa dacnicolor and designated PdT-1. The specification describes tryptophyllin-1 peptides and PdT-1 analogues which have a vasodilatory activity. Tryptophyllin-1 peptides are isolated from frog defensive skin secretions. Tryptophyllin-1 peptides of the invention are useful for preparing a medicament for treating disorders where vasodilation is beneficial, such as ischaemic hart disease, ischaemic disease of other organs or organ systems, vascular stenoses, occlusion to peripheral cosponates, or hypertension, and for increasing the transport of biologically active compounds across the blood-brain barrier, where the blood-brainy active compound is an anti-cancer drug. They are useful for promoting angiogenesis, for treating conditions of vascular promoten grafting, and for treating spinal cord injuries. They are also useful for treating vardiovascular disease, for increasing vasodilation, for treating spinal cord injuries. They are also useful for treating hypertension, for dilating arterial smooth muscle. In combination with other therapeutic agents, peptides of the invention are useful for treating disorders in the brain including central nervous
                                                                                                           vasodilation; ischaemic heart disease; ischaemic disease; vasodilation; ischaemic heart disease; rechaemic disease; vascular stenosis; occlusion; hypertension; blood-brain barrier; anti-cancer; angiogenesis, healing; transplant; graft; spinal cord injury; cardiovascular disease; arterial smooth muscle; central nervous system disorder; infection; inflammation; cancer; tumour; Hodgkin's disease; non-Hodgkin's lymphoma; multiple myeloma; haemacropoletic malignancy; glaucoma; pulmonary hypertension; stroke; atherosclerosis; asthma; ophthalmomlogic disease; renal failure; menstrual disorder; obstetric condition; wound; gastroenteric disease; anaphylactic shock; endotoxic shock; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated tryptophyllin peptide obtained from biologically active analog of Pachymedusa dacnicolor tryptophyllin-1, having vasodilatory activity, useful for treating conditions of vascular insufficiency e.g., ischemic
                                                       Nucleotide sequence of tryptophyllin-1 designated PdT-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 49; SEQ ID NO 17; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-FEB-2003; 2003GB-00002621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2004; 2004WO-IB000806
                18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                     Pachymedusa dacnicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-642491/62.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHAW C.
HIRST D.
CHEN T.
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(HIRS/)
(CHEN/)
(OROU/)
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O'rourke M;

Chen T,

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system disorder, bacterial, viral and fungal infections, inflammation and cancer, tumour, Hodgkin's disease, non-Hodgkin's lymphomas, multiple myeloma and haematopoietic malignancies. Tryptophyllin-1 peptides of the invention are also useful in treating glaucoma, pulmonary hypertension, stroke, atherosclerosis, asthma, ophthalmologic disease, renal failure, menstrual disorder, obsteric conditions, wound, gastroenteric disease, anaphylactic or endotoxic shock, etc.
                                                                                                                                                                                                                                                                                105
                                                                                                                                                                                                                                              44 AGCCCAAAGAIGITCACCTIGAAGAAAICCCTCTIACTCCTITCTICCTIGGGACCAIC 103
                                                                                                                                                                                                                                                                                                                104 AACTTATCTCTCTGTGAGGAAGAGAGAGAGATGCCGATGAAGAAGAAGAGAGATGATCTCGAA 163
                                                                                                                                                                                                                                                                                                                                      106 TCCATTTCCTTCTGTGATGAGGAAAAGACAGGATGACGATGAGGGAAAGAGAG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transgenic plants resistant to broad spectrum of pathogens useful for producing biologically active cationic peptides, comprises nucleic acid molecule encoding temporin and/or dermaseptin peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes a dermaseptin precursor polypeptide. The precursor is processed to produce two mature forms, dermaseptin b (AAB18725) and dermaseptin B (AAB18726). Dermaseptin has antibacterial activity, and inhibits fungal growth. Cationic peptides derived from temporins and dermaseptins are used to produce transgenic plants. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant; cationic peptide; pathogen resistance; ss.
                                                                                                                                                                                                                                                                                46 agaccadarargaarrrcirgaagagicgcirirccirgiccigirccicggrrcgir
                                                                                                                                                                                                              Gaps
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                                                                                                                                                                            DB 13; Length 341;
                                                                                                                                                                                                              Indels
                                                                                                                                           Sequence 341 BP; 132 A; 55 C; 74 G; 80 T; 0 U; 0 Other;
                                                                                                                                                                          14.2%; Score 46.8; DB 13; 60.0%; Pred. No. 0.0089; iive 0; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding a dermaseptin precursor polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "dermaseptin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
58. .294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA75749 standard; cDNA; 443 BP
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                                                                                                                                                                                              Local Similarity 60.0 les 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        166 GAAAAGAAAG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                      164 GAAAGGGATG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phyllomedusa bicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-647077/62.
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                                                                                                                                                                             Query Match
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                                                                                           defensive skin secretion;
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49 AGAACAAACATGGATATCCTGAAGAATCTCTTTTCCTTGTATTATTCCTTGGATTGGTT 108
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transgenic plants are useful for producing biologically active cationic
                                peptides such as temporins and dermaseptins in large quantities. The peptide confers broad spectrum pathogen resistance including enhanced resistance to both fungal and bacterial pathogens in the transgenic plants. The transgenic plants may be used in conventional agricultural applications such as food crops, medical and other applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                 Score 45; DB 3; Length 443;
                                                                                                                                                                                                                                                                                                                                                                                   35; Indels
                                                                                                                                                                                                                                            Sequence 443 BP; 211 A; 60 C; 77 G; 95 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 AACTTATCTCTCTGTGAGGAAGAGAGAGATGCCGATGAAGA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 recerricearcricidaagaagaaaaagaaaargaaga 149
                                                                                                                                                                                                                                                                                                                                                      0.03;
                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0.03
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7187/c
ABN77187 standard; cDNA; 403
                                                                                                                                                                                                                                                                                                                 13.7%;
65.3%;
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                                                                                                                                                                                                                                                                                                                                                                               66; Conservative
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                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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Sequences ABP31028-ABP35561 represent 4534 novel human proteins designated ORF (open reading frame) 1-4534, and sequences ABN75054-ABN79587 represent cDNAs encoding them. The invention also encompasses

Claim 1; Page 1323; 2508pp; English.

transplantation

Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ

Shimkets RA;

Leach MD,

2002-106200/14.

P-PSDB; ABP33161.

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polypeptides at least 80% identical to the ORFI-ORF4514 (collectively referred to as ORFX) proteins, polynucleotides at least 85% identical to the ORFX mucleic acid sequences, vectors and host cells comprising ORFX polynucleotides, the recombinant production of ORFX proteins, antibodies and polynucleotides, the recombinant production of ORFX proteins, antibodies and collections methods of screening for modulators of ORFX expression or appetite for ORFX proteins of the invention have a wide controlly, and methods of screening individuals for a predisposition to an OFFX associated disorder. The ORFX proteins of the invention have a wide confidence of biological activities, such as cytokine, cell proliferation, immune modulation, haematopoiesis regulation, tinsens of biological activity, hammal modulation, not inhibit activity, chemotractic/ chemokinetic activity, hammalory activity, thrombolytic activity, and mailinfective activity, and may also be involved in the determination of bodily characteristics, fertility and behaviour. ORFX proteins, or bodily characteristics, fertility and pobension and regeneration of organ transplantation, disorders such as sporiasis and benigh tumours, neurological disorders such as epoitasis and benigh tumours, or corgan transplantation, disorders of tissue growth and regeneration, diseases such as diabetes mellitus, hypothyroidism, and cholesteriol estructionage and probes, in the detection of ORFX genomic sequences to generate and probes, in the detection of ORFX genomic sequences the profuse and in drug screening. The ORFX protein may additionally be used to produce transgent animals as source of primers and probes, in the detection of ORFX proteins may additionally be used to produce transgent animals are sequenced. The organ of the pathyrole organ protein, and in drug screening. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 IGGAATIGGAAATCAICTAAIGIGGAAIGICATITAGCIAAAIGCACAICAAAIGICITA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 AAAGAAGAGATGTCTCGAAGAAAGGGTGTTGAAGTGGAAAAGCGATTTTTTCCAGTGA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 ATACAAATGATCAGTAGCAATATCTAGTGGCTCATGTGAAAGCAACTTTTTTCTCAGCTT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 TTGGAAGGATACTCAATGGTATTTTGGGAAAATAACCAAAAAAAGTTAAAACTTTGGAAA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233 TAGTAAAAATÁTTTCTAGATTTTTGAAGÁAGATÁAAGCÁTTAAAATTAÁTTÁGTATGAÁGA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 caaacagcracargacraragaaarargecararrcrcaargeacaragaargcrrca 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; biodiversity diseases; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antiulcer; osteopathic; immunosuppressive; antinflammatory; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.3%; Score 40.6; DB 6; Length 403; 51.4%; Pred. No. 0.47; tive 0; Mismatches 89; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 403 BP; 106 A; 71 C; 73 G; 153 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene therapy; chromosome 1; gene; ss.
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Matches 94; Conservative
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                 셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
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240 CAAAAAAGTTAAAACTTTGGAAATGGAA 268

Ното варіелв

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The invention relates to 971 novel human cDNA sequences (ADC29919-ADC30899) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99‡ identical with the invention and slow relates to nucleic acid sequences over 95 identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; and methods of against a polypeptide of the invention; and methods of polynucleotides or polypeptides of the invention; and methods of invention further discloses methods of peventing, treating or ameliorating a emdical condition; kits comprising polynucleotide probes and/or monoclonal antibodies for rarrying out the methods of the invention in methods for the identification of compounds that modulate the and/or monoclonal antibodies for rarrying out the methods of the invention of compounds that modulate the contig sequences corresponding to the cDNA sequences of the invention are corresponding to the cDNA sequences of the invention are defected in diagnostics, drug screening, forensics, gene mapping, in the contig education of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of data and other neurodegenerative diseases in and other reurodegenerative diseases, ansemia, placatel content of disorders, wounds, burns, ulcra, osteoporosis, autoimmune diseases or primers, and other neurodegenerating antibodies, as molecular weight markers, and in the recombinant production of a protain. The polypeptides are also useful in generating antibodies, as molecular weight markers, and in the recombinant production of a protain. Put mas are also useful in generating antibodies, as molecular weight markers, and in the present educates of the primers, and in the present educated of the primers and educating antibodies, as molecular weight markers, and in the propagation of t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 AGGAAGAGAGAGATGCCGATGAAGAAAGAGAGAGTGATCTCGAAGAAAGGGATGTTGAAG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 TGGAAAAGCGATTTTTCCAGTGATTGGAAGGATACTCAATGGTATTTTGGGAAAATAAC 239
                                                                                                                                                                                                                                                                                                     Wehrman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                        Weng G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 4414 BP; 1497 A; 828 C; 1167 G; 922 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68; Indels
                                                                                                                                                                                                                                                                                                     Zhang J, Ren F, Xue AJ, Zhao QA, Wang J,
Shosh M, Wang D, Ma Y, Asundi V, Wang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 776; 1185pp; English
                                                                                                                                                                                                                                                                                                                                                Haley-Vicente D, Drmanac RT;
                                                                                                                                                              24-SEP-2002; 2002WO-US030474.
                                                                                                                                                                                                          24-SEP-2001; 2001US-0324631P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-371981/35.
                                                                                                                                                                                                                                                                                                                        Ghosh M,
                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
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                                                                    WO2003029271-A2
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether progression of prostate cancer. (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) assessing the prostate cancer in a patient; (f) assessing the prostate cancer in a patient; (f) assessing the prostate cancer in a patient; (f) assessing the prostate cancer in a patient; (i) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2134 addakgaagaagaaaricagaagacricckgaarriccrircriagragaagaaaragaaa 2193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 AGGAAGAGAGAGATGCCGATGAAGAAGAAGAGATGATCTCGAAGAAAGGGATGTTGAAG 179
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                                                                                                                                                                                                                               Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
pharmacogenomic marker; gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.2%; Score 40.2; DB 5; Length 4804; 54.4%; Pred. No. 1.5;
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0; Mismatches
                                                                                                                                                                                            Human prostate expression marker cDNA 30190
   2340 CAAAAGATGAAAAAAAAATGGATAAAGAA 2368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 6542-6543; 11750pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monahan JE;
                                                                                          ВР
                                                                                          ABV30199 standard; cDNA; 4804
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2000US-0211314P.
2000US-0219007P.
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                                                                                                                                                              (first entry)
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16-MAR-2000;
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                                                                                                                             ABV30199;
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53.9%;

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The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequence complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis cytosine methylations. The parameters may difference serving as basis for diagnosis and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the S33 genomic sequences corresponding odd numbers are the complementary sequence of the corresponding odd numbered sequence (e.g. ID 2 and ID, ID 536 and ID 535, except for those whose partner sequence is missing). Note: The sequence data for this patent did not form part of the printed sequence diffication, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fragments of chemically modified genes associated with tumor suppressor genes and oncogenes, useful in designing primers and probes for analyzing diseases associated with cytosine methylation state e.g. cancer.
                                                                                                                                                                                                                                                                                                                  Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer;
tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
cytosine methylation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 56153 BP; 15738 A; 1002 C; 12377 G; 27036 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                            Tumour suppressor gene derived chemically modified sequence #520.
                                       2194 caaaagargaaaaagaaarggaraagaa 2222
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  CAAAAAAGTTAAAACTTTGGAAATGGAA 268
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                                                                                                                                               AAS46794 Btandard; DNA; 56153 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; 2000DE-01013847.
; 2000DE-01019058.
; 2000DE-01019173.
; 2000DE-01032529.
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                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                        AAS46794;
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Score 40; DB 4; Length 56153;

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                                                                                          9356 ACTCCAATAACCATTTTCTACAAATATCGTATTAATACTTAACAAATTTCAAATTTTAAA 9297
                                                                                                                                                                9296 АСАТАТТАААТТТТАААТТТТСАААТТААААТТАААААТАТСТСААССТАСАТАСАСТТА 9237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AnDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel disease. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvuleant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                            238 ACCAAAAAAGTTAAAACTTTGGAAATGGAATTGGAAATCATCTAAATGTGGAAATGTCATT
                                                        178 AGTGGAAAAGCGATTTTTTCCAGTGATTGGAAGGATACTCAATGGTATTTTGGGAAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fragment of chemically modified gene, useful sof diseases associated with abnormal cytosine
                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8781 BP; 2407 A; 65 C; 2093 G; 4216 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 1659; 32pp + Sequence Listing; German.
                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immune system associated gene SEQ ID NO: 1659.
                 70;
                                                                                                                                                                                                                                        9236 TACCTAAAACCCTAACAATATATTTTAAATA 9205
                                                                                                                                                                                                      298 TAGCTAAATGCACATCAAATGTCTTATAAAAA 329
   Pred. No. 4.2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berlin K;
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                                                                                                                                                                                                                                                                                                                               ABL33686 standard; DNA; 8781
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01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid comprising diagnosis and treatment methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Olek A, Piepenbrock C,
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Best Local Similarity
Matches 82; Conserv
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Matches 91; Conserv
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                                                                                                                                                                                                                                                                                                                                                                   ABL33686;
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148 AAGAGATGATCTCGAAGAAAGGGATGTTGAAGTGGAAAAGCGATTTTTTCCAGTGATTGG 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86 AAAAAAAATGAATAAGGTAACAGTGCAGAAAGTTACCAAAGTCAAAATAAAGGAAATGGC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ChK1 protein; SQ/TQ motif; isoelectric point; cell cycle progression; ds; nuclear localisation signal; DNA replication checkpoint; benign neoplasm; cell proliferative disorder; malignant neoplasm; human; claspin; gene.
                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                             The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal disgnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 AGGAGAAATTCTGGGCTATTAGGAAGTTTTATCACAAAACTTATTTTTTTCTATAATAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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11.7%; Score 38.6; DB 4; Length 466;
Best Local Similarity 52.1%; Pred. No. 1.8;
Matches 86; Conservative 0; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268 ATTGGAAATCATCTAATGTGGAATGTCATTTAGCTAAATGCACAT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 ATCTGTGATTTTCTATTTAAAACTTTTCTAGACTCCAAGCAAAAT 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 466 BP; 172 A; 64 C; 64 G; 166 T; 0 U; 0 Other;
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/*tag= a
/note= "Specifically claimed in claim
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/product= "Human Claspin protein"
799. .903
                                                                                                                                                                                                                                                                                                                       Claim 25; SEQ ID NO 5325; 654pp; English
                                                                                                                                                                                                                     Chen W, Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding human Claspin protein.
                                                                                                                                                                                                                                                                                             gene expression in human placenta.
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                                                                    04-FEB-2000; 2000US-0180312P.
26-MX-2200; 2000US-0207456P.
30-UJN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-023468PP.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC
                                          30-JAN-2001; 2001WO-US000663
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misc_feature
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               09-AUG-2001
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                                                                                                                                                                                                                   from base 1600001 (Methanococcus jannaschii circular
LOCUS AAV21209 Accession Aav21209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGACCTTAAAGATTCTTTGAAAAATGGATAAAGACATTGTAAAGATAACTTTTGATG 41830
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                                                         186 AGCGATTTTTCCAGTGATTGGAAGGATACTCAATGGTATTTTGGGAAAATAACCAAAAA 245
                                                                           AGAGAGATGCCGATGAAGAAGAAGAGATGATCTCGAAGAAAGGGATGTTGAAGTGGAAA 185
                            AAGTTAAAACTTTGGAAATTGGAAATCATCTAATGTGGAATGTCATTTAGCT 302
                                                                                                                                           AAGAAAGAAGAGATGATCTCGAAGAAAGGGATGTTGAAGTGGAAAAGCGATTTTTTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probe #5325 used to measure gene expression in human placenta sample.
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Pred. No. 7.4;
0; Mismatches 93; Indels 0:
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50.5%;
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Continuation (17 of 17) of AA
WP Sequence split into 17 frag
WP AAV21209 00
WP AAV21209 01
WP AAV21209 03
WP AAV21209 04
WP AAV21209 06
WP AAV21209 06
WP AAV21209 06
WP AAV21209 06
WP AAV21209 07
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WP AAV21209 11
WP AAV21209 12
WP AAV21209 11
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Matches
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Human, immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
    Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26254.
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                                                                                                             WO200157182-A2
                                                                                 Ното варіепв
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 The present invention relates to a new substantially pure Claspin polypeptide that specifically interacts with a ChK1 protein, having SQ/TQ motifies an isoelectric point of 4.5 and at least one nuclear localisation signal. The method of the invention is useful for identifying a compound that modulates cell cycle progression and for modulating cell cycle progression in a cell. The invention is useful for the proper operation of DNA replication checkpoint in the cell cycle. The method is also useful for treating a disorder associated with cell cycle progression e.g. cell proliferative disorder such as benign or malignant neoplasm. The molecules of the invention are also useful for detecting the altered levels of claspin expression. The present nucleic acid sequence encodes the human Claspin protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2026 AGGTAGAGAAAGAAGAAAAGAGGAAGAACTAGAGGAAGAGGAGGGGAAAGAAGAAGAGG 2085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2086 AGGAAGAAGAAGAAATCAGGAGACTGCAGAATTCCTTTAGTAGTAGAAATAGAAA 2145
                                                                                                                                                                                                                                                                                                                                                                                                                         Novel Claspin polypeptide specifically interacting with chK1 protein useful for identifying compound that modulates cell cycle progression and for treating cell proliferative disorder like neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 AGGAAGAGAGAGAGATGAAGAAAGAAGAAGATGATCTCGAAGAAAGGGATGTTGAAG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 TGGAAAAGCGATTTTTCCAGTGATTGGAAGGATACTCAATGGTATTTTGGGAAAATAAC 239
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*tag= c
note= "Specifically claimed in claim 9"
                                          'ttag= d
'note= "Specifically claimed in claim
2147. .2486
                                                                                             /*tag= e
/note= "Specifically claimed in claim
2964. .4756
                                                                                                                                         /*tag= f
/note= "Specifically claimed in claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2146 CAAAAGATGAAAAAGAAATGGATAAAGAA 2174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38.6;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                               (CALY ) CALIFORNIA INST OF TECHNOLOGY.
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ID AAK71442 standard, DNA, 23934 BP.
XX
AC AAK71442;
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DT 06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Fig 2; 97pp; English
                                                                                                                                                                                                                                                   17-OCT-2001; 2001WO-US032316
                                                                                                                                                                                                                                                                                  17-OCT-2000; 2000US-0241246P
                             .1543
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1 Similarity 53.7%;
80; Conservative
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P-PSDB; AAU97587.
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Best Local Similarity
Matches An. Comment
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PR 21-SEP-2000; 2000US-0234223 P.
PR 25-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-023493P.
PR 26-SEP-2000; 2000US-023493P.
PR 27-SEP-2000; 2000US-023534 P.
PR 27-SEP-2000; 2000US-023533 P.
PR 29-SEP-2000; 2000US-023533 P.
PR 29-SEP-2000; 2000US-023533 P.
PR 29-SEP-2000; 2000US-023533 P.
PR 29-SEP-2000; 2000US-02353 P.
PR 29-SEP-2000; 2000US-02353 P.
PR 29-SEP-2000; 2000US-02356 P.
PR 20-CCT-2000; 2000US-02356 P.
PR 20-CCT-2000; 2000US-02356 P.
PR 20-CCT-2000; 2000US-0235 P.
PR 20-CCT-2000; 2000US-0234 P.
PR 20-CCT-2000; 2000US-0234 P.
PR 20-CCT-2000; 2000US-024 P.
PR 20-CCT-2000;
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AAKS4951 to AAK64702 encode the human immune/haematopoletic antigen (I)

antino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)

CC activity, and can be used in gene therapy and vaccine production. (I)

CC proteins and polynucleotides may be used in the prevention, diagnosis and

CC treatment of diseases associated with decreased

expression by rectifying mutations or deletions in a patient's genome

CC expression by rectifying mutations or deletions in a patient's genome

CC expression by rectifying mutations or deletions in a patient's genome

CC expression by rectifying mutations or deletions in a patient's genome

CC supplement the patients own production of (I). Additionally, (I)

polynucleotides may be used to produce the secreted (I), by inserting the

CC nucleic acids into a host cell and culturing the cell to express the

CC cancers and cancer metafetses of haematopoletic-derived cells. AAK64703

CC cancers and cancer metafetses of haematopoletic-derived cells. AAK64703

CC cancers and cancer metafetses of haematopoletic-derived cells. AAK64703

CC sequences from the present invention. AAK54942 to AAK8759 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4567 İTTICCATAATAAATITITITITITAATITİTICIGAACCIGAGATGATGAAATGİÇİGİG 4508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4507 CTİCCCATTAAAACAĞGİTCAĞAGTACAACAĞAAACTTİĞAGGGAAAATAĞATAĞATAAİĞİ 4448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                447 cadaagtaadaagataaaatrccrcargardaagrcrcrgaagrcarcritaagrraar 4388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 TAACCAAAAAAGTTAAAACTTTGGAAATGGAATTGGAAATCATCTAATGTGGAATGTCA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 TTCACCTTCAAGAAATCCCTCTTACTCCTTGGGACCATCAACTTATCTCTC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 TGTGAGGAAGAGAGATGCCGATGAAGAAGAAGAGATGATCTCGAAGAAAAGGGATGTT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 GAAGTGGAAAAGCGATTTTTCCAGTGATTGGAAGGATACTCAATGGTATTTTGGGAAAA 235
                                                                                                                                                                                                                               Nucleic acids encoding human immune/hematopoletic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 26254; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 47.3%; Pred. No. 7.5;
Matches 116; Conservative 0; Mismatches 129; Indels 0;
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                                                                                                                                             Ruben SM
08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                             Barash SC,
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